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JOURNAL REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Deptment of Virology; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
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Shibahara,T., Tanaka,T. and Nakamura,Y.
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an cDNA sequencing project
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                                                                                                          /translation="MNKPITPSTYVRCLNVGLIRKLSDFIDPQBGWKKLAVAIKKPSG
DDRYNGPHIRREBALLQTGKS PYSELLEDWGTTMYCTVGGLVDLLIQNEFFAPASILLED
DAVKTANTLSKEAITVQKKOMPFCDKORTLTYCTVGGLVDLLIQNEFFAPASILLED
DAVFKTANTLSKEAITVQKKOMPFCDKORTLTYCTVGGLVDLLIQNEFFAPASILLED
SDTRFHSFSFYELKNVTNNFDERPISVGGNKMGEGGFGVVYKGYVNNTTVAVKKLAAM
VDITTEELKQQFDQEIKVMAKCQHENLVTLLGFSSDGDDLCLVYVYMPYKGSLLDRLSC
LDGTPFLSWHMRCKIAQGAANGINFLHENHHIHRDIKSANILLDEAFTAKISDFGLAR
ASEKFAQTVMTERIVGTAYAMAPEALRGBITPKSDIYSFGVULLBITGTAKISDFGLAR
ASEKFAQTVMTERIVGTAYAMAPEALRGBITPKSDIYSFGAVLLBITGTAKISDFGLAR
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                                                                                          QQLLQEMTAS"
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/protein_id="BAA91232.1"
/db_xref="GI:7020684"
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/cell_type="signet-ring cell carcinoma"
/clone_lib="KAT"
/note="cloning vector_pME18SFL3"
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/db_xref="taxon:9606"
/clone="KAT10395"
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/mol_type="mRNA"
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Alignment pred. No

Alignment Scores: Pred. No.: 1.11e-197 Score: Score: Percent Similarity: 99.78% Best Local Similarity: 99.78% Conservative: Mismatches: Mismatches: 1 Query Match: 99.83% Indels: 0	ALGETPELSWHARCKI AQGANAGINFLHENHHIHRDI KSANIILLDEAFTAKISDFGLAR ASEKFAQTVMTSRIVGTTAYMAPEALRGEITPKSDIYSFGVVLLEI ITGLPAVDEHRE PQLLLDIKEBIEDEEKTIEDYIDKKMNDADSTSVEAMYSVASQCLHEKKNKRPDIKKV QQLLQEMTAS" BASE COUNT 463 a 244 c 283 g 393 t	DDRYNQFHIRREBALLQTGKSPTSELLFWGTHWCTAGDLYDDLIQWEFAPASLLLP DDRYNQFHIRREBALLQTGKSPTSELLFWGTHWCTAGDLYDDLIQWEFAPASLLLLP DAVPKTANTLPSKEAITVQOKQMPFCDKDRTLWTPVQNLEQSYMPPDSSSPENKSLEV SDTRPHSFSTYELKNVTNNFDERPISVGSNWGEGGFGVVYKGYNNTTVAVKKAAM VDITTEELKQOFDQEIKVMAKCQHENLVELLGFSSDGDDLCLVYYYNPNGSLLDRLSC	/ID-ce"-nument IX-X-" /CODON_STATE=1 /proteIn_id="CAC60090.1" /proteIn_id="CAC60090.1" /db_xref="GI:15386463" /tb_colors		FEATURES LOCATION/QUALITIES SOURCE 1. 1383 /organism="Homo sapiens" /mol_type="genomic DNA" /mol_type="genomic DNA"	Irak-4: con Patent: Wo Tularik I	Eukaryota; Metazoa; Mammalia; Eutheria;	AX196260.1 . Homo sapien	RESULT 4 AX196260 AX196260 LOCUS LOCUS DEFINITION Sequence 2 from Patent WO0151641. ACCESSION AX196260	Qy 421 AlaAspSerThrSerValGluAlaMetTyrSerValAlaSerGlnCysLeuHisGluLys 440	Qy 401 GluGluIleGluAspGluGluLysThrIleGluAspTyrIleAspLysLysMetAsnAsp 420	uLeuAspIIeLys CTAGATATTAAA	361 ArgGlyGluIleThrProLysSerAspIleTyrSerPheGlyValValLeuLeuGluIIe	Qy 341 GlnThrValMetThrSerArgIleValGlyThrThrAlaTyrMetAlaProGluAlaLeu 360	
321 GluAlaPheThrAlaLysIleSerAspPheGlyLeuAlaArgAlaSerGluLysPheAla 	Qy 281 ProproLeuSerTrpHisNetArgCysLysILeAlaGInGlyAlaAlaAsnGlyIleAsn 300	61 ValTyrValTyrMetProAsnGlySerLeuLeuAspArgLeuSerCysLeuAspGlyThr 	Qy 241 GlnHisGluAsnLeuValGluLeuLeuGlyPheSerSerAspGlyAspAspLeuCysLeu 260	Qy 221 IleThrThrGluGluLeuLysGlnGlnPheAspGlnGluIleLysValMetAlaLysCys 240	QY . 201 TyrLysGlyTyrValAsnAsnThrThrValAlaValLysLysLeuAlaAlaMetValAsp 220	Qy 181 AspGluArgProIleSerValGlyGlyAsnLysMetGlyGluGlyGlyPheGlyValVal 200	Qy 161 SerAspThrArgPheHisSerPheSerPheTyrGluLeuLysAsnValThrAsnAsnPhe 180	Qy 141 LeuGluGlnSerTyrMetProProAspSerSerPeroGluAsnLysSerLeuGluVal 160	Qy 121 GlnGlnLysGlnMetProPheCysAspLysAspArgThrLeuMetThrProValGlnAsn :40	Qy 81 ValGlyAspLeuValAspLeuLeuIleGlnAsnGluPhePheAlaProAlaSerLeuLeu 100	CRI GI	Qy 41 LysProSerGlyAspAspArgTyrAsnGlnPheHisIleArgArgPheGluAlaLeuLeu 60	pPheIleAspProGlnGluGlyTrpLy 	ysProIleThrProS AACCCATAACACCAT	DB: 6 Gaps: 0 US-10-001-254-16 (1-460) x AX196260 (1-1383)

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NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Wirology and Human Genome Center, Institute of Medical Science, This work of Tokyo (Act of
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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lomo sapiens cDNA FLJ20521 tis,
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AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT 180
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ASEKFAQTVMTSRIVGTTAYMAPEALRGEITPKSDIYSFGVVLLEIITGLPAVDEHRE
PQLLLDIKEEIEDEEKTIEDYIDKKWNDADSTSVEAMYSVASQCLHEKKNKRPDIKKV
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/db_xref="G1:7020684"
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SDTRFHSFSFYFELKNVTNNFDERFISVGGKNGEGGFGVVYKGYVNNTTYAVKLAAM
VDITTEELKQQFDQEIKVMAKCQHENLVELLGFSSDGDDLCLVYVYMPDGSLLDRLSC
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/cell_type="signet-ring cell carcinoma"
/clone_lib="KAT"
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|mol_type="mRNA"
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ra,T., Tanaka,T.,
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Tularik Inc.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                        GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGCTGGTGATCTTTGTGGATCTTTTTG
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//db_xref="G1:15386463"
//db_xref="G1:15386463"
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/briteelkoqefdoeikvmakcohenleitglfksdivsfgvylleiitglpaudehre
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Best Local Similarity:
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                 JOURNAL
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ORGANISM
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                                                                                                                                                                                                                                                                                       Homo sapiens putative exotein complete cds.
                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2817)
Scanlan,M.J., Gordan,J.D., Williamson,B., Stockert,E., Bander,N.H.
Scanlan,M.J., Gordan,J.D., Williamson,B., Stockert,E., Bander,N.H.
                                                                                                                                      Jongeneel, V., Gure, A.O., Jager, D.,
                                                                                                                                                                                                                                                                            AF155118.1 GI:5360130
2 (bases 1 to Scanlan, M.J., C
                                                                    renal-cell carcinoma Int. J. Cancer 83 (4),
                                                                                                      Antigens recognized by autologous antibody
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DDRYNQFHIRRFEALLQTGKSFTSELLFDWGTTNCTVGDLVDLLIONEFFAPASILLP
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SDTRFHSFSFYELKNVTMNFDERFISVGGMVGEGGFGVVYXGTVNNTTVAVKKLANA
VDITTEELKQQFDQEIKVMAKCQHENLVELLGFSSDGDDLCLVYVYMPNGSLLDRLSC
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asekfaqtvmtsrivgttaymapealrgeitpksdiysfgvvlleiitglpavdehre
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| mol_type="genomic DNA"
| db_xref="taxon:9606"
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 Gordan, J.D.,
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 Williamson, B.,
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   Stockert, E.,
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Chen, Y.-T.
   Bander, N.H.,
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RESULT 7
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Direct Submission
Submitted (28-MAY-1999) Ludwig Institute, Sloan-Kettering Institute, 1275 York Ave, New York, NY 10021, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jongeneel, V., Gure, A.O., Jager, D., Jager, E., Knuth, A., Chen, Y.-T. and Old, L.J.
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Watanabe, K., Kumagai, A., Itakura, S., Yamaz
Ota, T., Suzuki, Y., Obayashi, M., Nishi, T.,
                                                                                                   AK000528.1 GI:7020683 oligo capping; fis (full insert sequence) Homo sapiens (human)
                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                         AK000528
Homo sapiens cDNA FLJ20521 F15,
                                                                                                                                                          AK00052E
                                                                                    Homo sapiens
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LDGTPPLSWHMRCKIAQGAANGINFLHENHHIHRDIKSANILLDEAFTAKISDFGLAR
ASEKFAQTVMTSRIVGTTAYMAPEALRGEITEKSDIXSFGVVLLEIITGLPAVDEHRE
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/product="putative protein kinase NY-REN-64 antigen"
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/db_xref="GI:5360131"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sugano, S., Suzuki, Y., Ot
Shibahara, T., Tanaka, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Deptment of Victology; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
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                                                                                                                                                                                                                                                                                                                  ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 113
                                                                                                                                                                                                                                                                                                                                          ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20
IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro
                                                                                          GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
                                                                                                                                                  AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
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DAVPKTANTLSKEAITVQQKCMPFCDKDRTLMTPVQNLEQSYMPDSSSSPENKSLAV
SDTRFHSFSFYELKNVTNNFDERPISVGGNKMGEGGFGVVYKGYVNNTTVAVKKLAAM
VDITTEBLKQQFDQEIKWAKCQHENLVELLGFSSDEDDLCLVVYYMPNGSLLDRLSC
LDGTPPLSWHRFCKIAQGAANGINFLHENHIRDIKSANILLDEAFTAKISDFGLAR
ASEKFAQTVMTSRIVGTTAYWAPEALRGEITEKSDIYSFGVULLEIITGLBAVDEHRE
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="KAT"
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T. and Nakamura,Y.
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Patent: WO 0151641-A 2 19-JUL-2001;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 318
                   IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro
                                                                                                                                  AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
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DDRXNGPHIRREBALLQTGKSSTSELLFDWGTTNCTAGDLVDLLIQUEFFAPASLLLP
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ASEKFAQTVMTSRIVGTTAYMAPEALRGEITPKSDIYSFGVVLLEIITGLPAVDEHRE
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/db_xref="taxon:9606"
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RESULT

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Command line parameters:

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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEU TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

284 bp mkNA linear EST 13-NOV-19 zn75g05.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens CDNA Clone IMAGE:564056 5', mRNA sequence

EST 13-NOV-1996

AA114228 AA114228.1 GI:1668121

ACCESSION VERSION

KEYWORDS

SOURCE ORGANISM

REFERENCE

Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 284)

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Percent Similarity:
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Email: est@watson.wustl.edu
This_clone is available royalty-free through LLNL; contact the
This_clone is available royalty-free through LLNL; contact the
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Seq primer: -28M13 rev2 from Amersham.
Location/Qualifiers
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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//dev_stage="Nera-2 neuroepithelial cells"
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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DKFZp686K18112_5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: ATCC
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Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysProSerGlyAspAspArgTyrAsnGlnPheHisIleArgCys 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAACCATCTGGTGATGATAGATACAATCAGTTTCACATAAGATGC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGCTGTCAGATTTTATGGATCCTCAAGAAGGATGGAAGAAGTTAGCTGTAGCTATTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGAACAAACCCATAACACCATCAACATATGTGCGCTGCCTCAATGTGGGACTAATTAGG 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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re greater than or equal to the score of the result being printed,
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10.8 1557

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Gapop 10.0 , Gapext 1.0
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294
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backtiles1.seq:*
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     US-09-398-395A-51
US-09-887-586A-51
US-09-895-752-51
US-09-903-0128-51
US-09-903-0128-51
US-08-545-528D-1
US-08-61-527-90
US-09-734-674-3
US-09-791-211-10
US-09-91-211-10
US-09-107-532A-3535
US-09-107-532A-3535
US-09-107-532A-3535
US-09-114-0101-1614
US-09-114-0101-1614
US-09-620-312D-120
4 US-08-916-4218-1
US-08-455-745-1
US-08-465-11
US-09-679-198-60
US-09-679-409-1
US-09-679-409-1
US-09-328-352-897
US-08-929-329-3
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Sequence 51, Appl
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Sequence 90, Appl
Sequence 10, Appl
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Sequence 120, App
Sequence 1614, App
Sequence 17, Appl
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Sequence 2, Appli	Sequence 22 App	Sequence 20, App.	Sequence 24, App.	Sequence 172, App	Sequence 4, Appli	•	•	Sequence 35, Appl	•	•	•	•	Sequence 34, App	•	Sequence 20, App	•	Sequence 20, App

ALIGNMENTS

Qy Db	Qy	Qy Db	Qу	Qy db	Query M Best Lo Matches	RESULT 1 Sequen Sequen Patent APPLI	
241 ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 294	181 GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG 240 	121 AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT 180 	61 CAAGAAGGATGGAAGAAGTTAGCTGTAGCTATTAAAAAACCATCTGGTGATGATAGATA	1 ACATAIGIGCGCTGCCTCAAIGITGGACTAATTAGGAAGCTGTCAGATTTIATTGAICCT 60 	ry Match 100.0%; Score 294; DB 4; Length 833; : Local Similarity 100.0%; Pred. No. 3.4e-82; :hes 294; Conservative 0; Mismatches 0; Indels 0; Gaps	WESULT 1 US-09-166-350-10 Sequence 10_Application US/09166350A Patent No. (644063) GENERAL INFORMATION: APPLICANT: Scanlan, Matthew APPLICANT: Stockert, Elisabeth APPLICANT: Old, Lloyd APPLICANT: Old, Lloyd APPLICANT: Old, Lloyd APPLICANT: Muth, Alex TITLE OF INVENTION: Renal Cancer Associated Antigens and TITLE OF INVENTION: Wess Therefor FILE REFERENCE: L0461/7051 CURRENT APPLICATION NUMBER: US/09/166,350A CURRENT FILING DATE: 1998-10-05 EARLIER APPLICATION NUMBER: US/09/166,350 EARLIER FILING DATE: 1998-10-05 NUMBER OF SEQ ID NOS: 35 SEQ ID NO 10 LENGTH: 833 TYPE: DNA ORGANISM: Homo sapiens US-09-166-350-10	

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Result
No.
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-MODEL-frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USFTO_spool/US10001254/runat_16012004_152425_19740/app_query.fasta_1.1109
-Q=/cgn2_1/USFTO_spool/US10001254/runat_16012004_152425_19740/app_query.fasta_1.1109
-DB=Issued Patents_NA -QFMT=fastap_SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Bits_START=1 -END=-1 -MATRIX=blosum62 -TRANS=bluman40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct_THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext_-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MMAP_-LARGEQUERY_-NEG_SCORES=0 -WAIT_-DSPBLOCK=100 -LONGLOG_DS-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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      833
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                     US-09-166-350-10

US-09-135-232-1

US-09-833-549-1

US-09-830-560-1

US-08-980-060-1

US-08-980-060-3

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US-09-307-185-3

US-09-217-185-14

US-09-234-393-26
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ALIGNMENTS

US-09-166-350-10

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; SEQ ID NO 10
; LENGTH: 833
; TYPE: DNA
; ORGANISM: Homo s
US-09-166-350-10
                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                             APPLICANT: Scanlan, Matthew
APPLICANT: Chen, Yao
APPLICANT: Chen, Yao
APPLICANT: Old, Lloyd
APPLICANT: Old, Lloyd
APPLICANT: Jager, Elke
APPLICANT: Winth, Alex
TITLE OF INVENTION: Renal Cancer Associated An
TITLE OF INVENTION: Uses Therefor
FILE REFERENCE: L0461/7051
CURRENT APPLICATION NUMBER: US/09/166,350A
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: US 09/166,350
SEO ID NOS: 35
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
US-10-001-254-6 (1-98)
                                                                                                                   Score:
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Patent No. 644063
GENERAL INFORMATION:
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Mismatches:
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Query
          US-09-863-549-1
; Sequence 1, Application US/09863549
; Patent No. 6576444
; GENERAL INFORMATION:
                                                                           RESULT 3
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US-09-135-232-1
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SEQ ID NO 1
LENGTH: 2288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09135232
Patent No. 6262228
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CURRENT FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
FILE REFERENCE: T98-019
APPLICANT: Cao, Zhaodan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: CDS
LOCATION: (64)..(1851)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: human
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Y Match:
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31.51%
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Matches:
Conservative:
Mismatches:
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Gaps:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1,
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TYPE: DNA
ORGANISM: human
FEATURE:
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APPLICANT: NI, JI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods FILE REFERENCE: T98-019
CURRENT APPLICATION NUMBER: US/09/863,549
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 09/135,232
PRIOR FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (64)..(1851)
                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: PM PC COMPATIBLE
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
             ATTORNEY/AGENT INFORMATION: NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                               APPLICANT: FENG, PING
APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HUMAN IRAK-2
                                            APPLICATION NUMBER: FILING DATE: Herewichassification: 43:
                                                                                                                                                                                                             STATE: D.C.
REGISTRATION NUMBER:
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Indels:
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Matches:
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Perfect score:
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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US-08-980-060-3

US-09-307-185-3

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ALIGNMENTS

US-09-166-350-10

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Percent Similarity:
Best Local Similarity:
                  Best Local S
Query Match:
                                                                   Score:
                                                                                  Pred.
                                                                                               Alignment Scores:
                                                                                                                               ; ORGANISM: Homo sapiens US-09-166-350-10
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Scanlan, Matthew
APPLICANT: Chen, Yao
APPLICANT: Stockert, Elisabeth
APPLICANT: Old, Lloyd
APPLICANT: Jager, Elke
APPLICANT: Knuth, Alex
                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Applicate Patent No. 6440663 GENERAL INFORMATION:
                                                                                                                                                                                                                                       TITLE OF INVENTION: Renal Cancer Associated TITLE OF INVENTION: Uses Therefor FILE REFERENCE: 1.0461/7051
CURRENT APPLICATION NUMBER: US/09/166,350A CURRENT FILING DATE: 1.998-1.0-05
EARLIER APPLICATION NUMBER: US 09/166,350
EARLIER FILING DATE: 1.998-1.0-05
                                                                                                                                                            TYPE: DNA
                                                                                                                                                                           LENGTH: 833
                                                                                  No.:
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Gaps:
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Matches:
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US-09-166-350-10 (1-833)

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RESULT 2
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Sequence 1, Application I
Patent No. 6576444
GENERAL INFORMATION:
APPLICANT: Cao, Zhaodan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/135,232
CURRENT FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
FILE REFERENCE: T98-019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: human FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                          8 ValGlyLeuIleArgLysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeu
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Matches:
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US-08-980-060-1
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Best Local Similarity:
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CURRENT APPLICATION NUMBER: US/09/863,549
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 09/135,232
PRIOR FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 2
COCRUMENT OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
                                                                                                          ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
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LOCATION: (64
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ORGANISM: human
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               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NI, JIAN
APPLICANT: FENG, PING
APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                      STREET: 1100 NEW CITY: WASHINGTON
                                                                       APPLICATION NUMBER: US
                                                                                                                                                                                                                                                 COUNTRY: USA
NAME: STEFFE, ERIC REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196
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RESULT 5
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application Patent No. 6222019
                                                                                                   ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                          CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, K
                                                                                                                                                                                                                                                                                                              APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.:
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                                                                         APPLICATION NUMBER: FILING DATE:
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Best Local Similarity:
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Patent No. 596542
        MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,060
FILING DATE: Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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FENG, PING
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DIXIT, VISHVA N
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Matches:
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Best Local Similarity:
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Patent No. 622201
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 3459 base pairs
                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/307,185
FILING DATE:
                                                                                                                                                                                                                                                                                                        APPLICANT: FENG, PING
APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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LOCATION:
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TYPE: nucleic acid
                                 CLASSIFICATION:
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REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
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 US/08/980,060
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US-09-307-185-3
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                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5965421
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14,
                                                                        COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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INFORMATION FOR SEQ ID NO:
   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/980,060 FILING DATE: Herewith CLASSIFICATION: 435
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REFERENCE/DOCKET NUMBER: 14:
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                    STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                                                                                          CITY: WASH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 TGGTGGTGGGGGATGCGGCAGGCCÁCCGTCCAGCAACTTGTGGACCTCCTGTGCCGCCTG 276
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DEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08980060
                                                                                                                                                                                                                       E: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. 1100 NEW YORK AVENUE, N.W., SUITE 600
                                                                                                                                                                                                                                                                                                      FENG, PING
MUZIO, MARTA
DIXIT, VISHVA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3459 base pairs
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(202) 371-2540
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RESULT 9
US-09-307-185-14/c
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 622201
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              REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
TELECOMMUNICATION INFORMATION:
                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                      APPLICATION NUMBER: 1
                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: NI, JIAN
APPLICANT: FENG, PING
APPLICANT: MUZIO, MARTA
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 479 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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REFERNCE/DOCKET NUMBER: 14.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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                                                                                                                                                           CLASSIFICATION:
                                                               NAME: STEFFE, ERIC K.
                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                         STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                          CITY: WASHINGTON
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TELEPHONE:
                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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(202) 371-2600
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78.50
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APPLICANT: Freiberg, Christoph
APPLICANT: Perret, Xavier Philippe
APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence
Patent No. 6475793
TITLE OF INVENTION: Plasmid
FILE REFERENCE: CARPO068
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                                                                                                                       US-10-001-254-6 (1-98) x US-09-214-808-1 (1-536165)
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Best Local Similarity:
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SEQ ID NO 1
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1997-
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                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Rhizobium
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No.:
                                                                                                                                                                                                                                              No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 479 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
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                                                    INFORMATION:
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36 ---GlyAspAspArg---TyrAsnGlnPheHisIleArgArgPheGluAlaLeuLeuGln 53
                                                                                 18 IleAspProGlnGluGlyTrp---LysLysLeuAlaValAlaIleLysLysProSer---
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US-09-234-393-26
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Query Match:
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SOFTWARE: PatentIn Ver.
SEQ ID NO 26
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TYPE: DNA
ORGANISM: Abies
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CURRENT FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: 60/072,204
EARLIER FILING DATE: 1998-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SESQUITERPENE SYNTHASES TITLE OF INVENTION: AND METHODS OF USE FILE REFERENCE: WSUR113345
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APPLICANT: Jetter, Reinhard
APPLICANT: Steele, Christopher L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Croteau, Rodney B
APPLICANT: Crock, John E
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                  792 GGTGAACATTTACCAATCGACATTCTGGAGCAAATATTCTTGCCCTCCAGGTTCCACCAT
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                                                         83 AsnGlu-----
                                                                                                                                  66 TrpGlyThrThrAsn------CysThrValGlyAspLeuValAspLeuLeuIleGln
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                                                                                               AATGGCACCAAACACTGGGATGTGTATTG---AATTTGATTCCGCTTCTGTTAATG
                                                                                                                                                                             CTGCAAGATGCGGAATGGATAGCCACTGGACATGTCCCCACCTTTGATGAGTACTTGAAT
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                                                         ---PhePheAlaPro----
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; OTHER INFORMATION: Clone
US-09-360-545-19
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RESULT 13
US-09-865-171-26
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Best Local Similarity:
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LENGTH: 1416
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CURRENT FILING DATE: 1999-07-26
EARLIER APPLICATION NUMBER: 60/052,249
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: PCT/US98/14528
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APPLICANT: Bohlmann, Jorg
APPLICANT: Steele, Christopher L
APPLICANT: Phillips, Michael A
TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1998-07-10 NUMBER OF SEQ ID NOS: 107
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NAME/KEY: CDS
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Sequence 49, Application US/092:
Patent No. 6265639
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Crock, John E
APPLICANT: Bohlman, Jorg
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; ORGANISM: Abies
US-09-865-171-26
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Patent No.
APPLICANT: Jetter, Reinhard
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
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PRIOR FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
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CURRENT FILLING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/234,393
PRIOR FILLING DATE: 1999-01-20
PRIOR FILLING DATE: 1999-01-20
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APPLICANT: Steele, CStristopher L
TITLE OF INVENTION: SESQUITERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS),
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: WSUR117468
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APPLICANT: Crock, John
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Patent No. 6265639
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                              APPLICANT: Croteau, Rodney B
APPLICANT: Crock, John E
APPLICANT: Bohlman, Jorg
APPLICANT: Bether, Reinhard
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: SESQUITERPENE SYNTHASES
TITLE OF INVENTION: AND METHODS OF USE
                      FILE REFERENCE: WSUR113345
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EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
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LOCATION: (4)..(1782)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1321 AATGGCACACCAAACACTGGGATGTGTGTATTG---AATTTGATTCCGCTTCTGTTAATG 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1261 CTGCAAGATGCGGAATGGATAGCCÁCTGGACATGTCCCCÁCCTTTGATGAGTACTTGAAT
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APPLICATION NUMBER: US/09/234,393A
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                                                                                                                                                                                                                                                                                                                                                                     GGTGAACATTTACCAATCGACATTCTGGAGCAAATATTCTTGCCCTCCAGGTTCCACCAT 143;
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                                                                                                                                                                                                               Application US/09234393A
                                                                                                                                                                                                                                                                                                                             ----AlaSerLeuLeuLeuProAspAla
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, NAME/KEY: CDS

, LOCATION: (4)..(1782)

US-09-234-393-51
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LENGTH: 1785
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EARLIER APPLICATION NUMBER: 60/072,204
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: computer-generated nucleic acid sequence encoding
OTHER INFORMATION: gamma humulene synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                             1438 CTCATTGAATTGGCTTCCAGGCTCGTCGATGACGCG 1473
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                                                                                                                                                                                                                                1321 AATGGCACACCAAACACTGGGATGTGTGTTTG---AATTTGATTCCGCTTCTGTTAATG 1377
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                                                                                                                                                       1378 GGTGAACATTTACCAATCGACATTCTGGAGCAAATATTCTTGCCCTCCAGGTTCCACCAT 1437
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Matches:
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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USFTO gool/US10001254/runat 16012004 152423 19714/app query.fasta_1.1109
-Q=/cgn2 1/USFTO gool/US10001254/runat 16012004 152423 19714/app query.fasta_1.1109
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-DOCALIGN=200 -THR SCORE=500 -MINLEN=0 -MAXIEN=2000000000
-USER=US10001554 @CGN 1 1 5671 @runat 16012004 152423 19714 -NOPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

AX431296

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AUTHORS
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                                         Unknown
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Mammalia; Eutheria; Primates;
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                                                     Unknown.
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                                                                                                                                                                     ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 294
                                                                                                                                                                                                                         GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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 Chen, Y.-T.,
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Catarrhini; Hominidae;
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 Old, L.J.,
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 Jager, E.
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                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                               Roth, W. and Stenner-Liewen, F.
Novel death domain proteins
Patent: WO 0240680-A 15 23-MAY-2002;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/note="unnamed protein product"
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DAVPKTNTLPSKEAITVQQKMPFCDKDFTMTPVQNLEQSYMPPDSSSENKSLEV
SDTRFHSFSFYELKNVTNNFDERPISVGGNKGEGGGGVVYKGYVNNTTVAVKKLAAM
VDITTEELKQQFDQEIKVMAKCQHENLVELLGFSSDGDDLCLVVVYMPNGSLLDRLSC
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                                                                                                                                            /organism="Homo sapiens"
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/db_xref="taxon:9606"
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                             Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 19 Row: n Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7705840. Location/Qualifiers
                                                                                                                                               CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amaddan@systemsbiology.org Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ш
                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (31-AUG-2001) National Institutes of Health, Mammalian Submitted (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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BC013316
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                 REFERENCE
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Best Local Similarity:
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                              Roth, W. and Stenner-Liewen, F.
Novel death domain proteins
Patent: WO 0240680-A 27 23-MA
BURNHAM INST (US)
                                                                                                                                                                                                                               Sequence 27
AX431318
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                AX431318.1
                                                                                                 Pawlowski,K.,
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517.00
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                                                                                               Fiorentino, L.,
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Matches:
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1629 98 0 0

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PAT 28-JUN-2002

388 98

> 80 334

274 60 214 40 154 20

Lee, S.H.,

Reed, J.C.,

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SOURCE

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468
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                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2817)

Scanlar, M.J., Gordan, J.D., Williamson, B., Stockert, E., Bander, N.H Jongeneel, V., Gure, A.O., Jager, D., Jager, E., Knuth, A., Chen, Y.-T.
2 (bases 1 to 2817)
Scanlan, M.J., Gordan
                                                                                                                                                                                                                                                                                                                                            Homo sapiens putative complete cds.
                                                                           Antigens recognized by autologous antibody renal-cell carcinoma Int. J. Cancer 83 (4), 456-464 (1999)
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                                                              99438124
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      IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuLeuProAspAlaValPro
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                                                                                                                                      Old, L.J.
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BOTRFHSFSFYELKNVTNNFDERPISVGGNKMGEGFGVVYKGVNNTTVAVKKLAAM
VDITTEELKQOPQDGIKWMAKCQHENLVELLGFSSDGDDLCLLYVYVMPMSGLLDRLSC
LDGTPPLSWHMRCKIAQGAANGINFLHENHHIHRDIKSANILLDEAFTAKISDFGLAR
ASEKFAQTVMTSRIVGTTAYMAPEALRGEITPKSDIYSEGVVLLEIITGLPAVDEHRE
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/mol_type="genomic DNA"
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   Gordan, J.D.,
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     Bander, N.H.,
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(sites)
Watanabe,K.)
Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,
Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Ta
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Submitted (28-MAY-1999) Ludwig Institute, Sloan-Kettering
Institute, 1275 York Ave, New York, NY 10021, USA
                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (human)
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AK000528.1 GI:7020683
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Homo sapiens cDNA FLJ20521 118,
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and Old,L.J.
                                                                                                                 Homo sapiens
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ASEKFAQTVMTSRIVGTTAYMAADEALRGEITPKSDIYSFGVVLLEIITGLPAVDEHRE
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|mol_type="mRNA"
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NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA library sequencing: Research Association for Blotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, Virology and Human Genome Center, Institute of Medical Science,
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Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.
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                                                                                      GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                  IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro
                                                                                                 GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGCTGGTGATCTTGTGGATCTTTTG
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Suzuki, N., Suzuki, S., Duncan, G.S., Millar, D.G., Wada, T.,
Mirtsos, C., Takada, H., Wakeham, A., Itie, A., Li, S., Pennin,
Wesche, H., Ohashi, P.S., Mak, T.W. and Yeh, W.C.
Severe impairment of interleukin-1 and Toll-like receptor
signalling in mice lacking IRAK-4
Nature 416 (6882), 750-756 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="IRAK4"
                                                                                                                                                             2.56e-60
513.00
58.98%
98.98%
99.23%
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                                                                                                                                                                                                                                                                                                         283
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                                                                                                                                        Length:
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                         393
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1 kinase 4
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4 (IRAK4)
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REFERENCE
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AX196262
LOCUS
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Best Local Similarity:
Query Match:
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ORGANISM
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Mus sp.
Eukaryota;
                  21 GlnGluGlyTrpLysLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 40
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Patent: WO 0151641-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
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SDTRFHSFSHELKSITNNFDEQPASAGGNRWGEGGFGVVYKCCVNNTIVAVKKLGAM
VEISTEELKQQFDGIKVMATGQHENLEHHHHRDIKSANILLDKDFTAKISDFGLAR
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ASARLAQTVMTSRIVGTTAYMAPEALRGEITPKSDIYSFGVVLLELITGLAAVDENRE
PQLLLDIKEEIEDEEKTIEDYTDEKMSDADPASVEAMYSAASQCLHEKKURRPDIAKV
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392 c
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/more="murine IL-1 receptor-associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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Patent WO0151641.
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                                                                                                                                                 Gaps:
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Percent Similarity:
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Query Match:
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ORGANISM
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AF445803
LOCUS
                                                                                                                                             Score:
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    US-10-001-254-6 (1-98) x AF445803
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AF445803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li,S., Strelow,A., Fontana,E.J. and Wesche,H. Direct Submission
Submitted (08-NOV-2001) Biology I, Tularik In South San Francisco, CA 94080, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li,S., Strelow,A., Fontana,E.J. and Wesche,H. IRAK-4: a novel member of the IRAK family with the properties of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF445803.1 GI:20219011
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/note="protein kinase"
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163. .1542
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DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
                                       cDNA Library Preparation: Yulan Piao and Minoru Ko
                                                                                                          NIH-MGC Project URL: http://mgc.Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                Submitted (30-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC051676 2431 bp mRNA linear ROD 10-JUN-2003 Mus musculus interleukin-1 receptor-associated kinase 4, transcript variant 1, mRNA (CDNA clone MGC:60994 IMAGE:30017484), complete
                                                                                        Tissue Procurement: Minoru
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Eutheria; Rodentia;
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Mus.

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US-10-001-254-6 (1-98) x BC051676 (1-2431)
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Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                          1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 111 Row: i Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23943897.

Location/Qualifiers
                                GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu
                                                                                                            AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer
                                                                                                                                                                              CAAGAAGGGTGGAAGAATTAGCAGTAGCTATCAAAAAGCCGTCCGGCGACGACAGATAC
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/translation="makeltestyirklungiirklsdeidpoegwkklavaikkpsg/
/translation="makeltestyirklungiirklsdeidpoegwkklavaikkpsg/
Drynofhirrealtofksptcellfdwgttnctvgdlundlungielfaratlle
Davpotykslerealtvaothgoeoekdrtsvmmeklehscepedsssednrsves
SDTRFHSFSFHELKSITNNFDEOPASAGGNRMGEGGFGVVYKGCVNNTIVAVKKLGAM
VEISTEELKOOFDOEIKWATCOHENLYCLLOFSSDINLCLVXAYMPMGSLLDRLSC
LDGTPPLSWHTRCKVAGGTANGIRFLHENHIHEDIKSADILLDRDFTAKISDFGLAR
LDGTPRLSWHTRCKVAGGTANGIRFLHENHIHEDIKSADILLLDRDFTAKISDFGLAR
ASARLAOTVMTSRIVGTTAYMAPEALRGEITPKSDIYSFGVVLLELITGLAAVDENRE
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/tissue_type="Embryo, whole, mouse, 7.5-dpc"
/clone_lib="NIA Mouse 7.5-dpc Whole Embryo cDNA Library
(Lone)"
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/db_xref="LocusID:266632"
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/strain="C57BL/6J"
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                                                                                                          BC045381 1719 by Danio rerio, Similar to interlectione MGC:55553 IMAGE:2642773,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 1719)
                                                  Danio rerio
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Mammalia; Eutheria; Primates;
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                                                           Danio rerio (zebrafish)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
102 c 97 g 13
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Tissue Procurement: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
cDNA Library Preparation: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 101 Row: m Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Direct Submission
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                                                                                                                              GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr
                      ACACAGATGCACATGAGGCGGTTTGAAGCATGCGTCCTGCAGGGAAAGAGTCCCACCATG
                                                        AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
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HSVCHAHTGSVWCEEAAPASAVCLQACEITQTVEDNSNKPQKISKFVEDDSNKPVQEQ
ELFVEPDSSSGAQESSWDSSQGFHTFSLHELTAMTQHWDERPLSDGGCRLGSGGFGVV
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/db_xref="GI:28278876"
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(tissue_type="Whole body, adult, (one male including unfertilized eggs)"
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db_xref="taxon:7955"
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/gene="IRAK4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1705 NE Pacific, Seattle, WA 98195, USA
To cite this work please use: SeattleSNPs. NHLBI HL66682 Program
for Genomic Applications, UW-FHCRC, Seattle, WA (URL:
http://pga.gs.washington.edu).
Location/Qualifiers
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Homo sapiens interleukin-1 receptor-associated
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Rajkumar, N., Toth, E.J., Yi, Q. and
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25244. .25427,26599. .26661,29336. .29494,29617. .31033)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carrington, D.P., Ozuna, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nickerson, D.A
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'replace="a"
                                                                                                                frequency="0.01"
replace="t"
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frequency="0.04"
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replace="t"
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replace="g"
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_type=dispersed
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              Percent Similarity:
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Query Match:
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7074. .7366
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5821
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/replace=""
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/replace="a"
                                                                                                        replace="g"
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rpt_type=dispersed
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rpt_type=dispersed
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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49
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	Qy 85 PhePheAlaProAlaSerLeuLeuLeuPro 94
14271	Db 14212 GACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTGATCCAAAATGAA 14271
84	Qy 65 AspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeuIleGlnAsnGlu
14211	Db 14152 TTAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCTGAATTACTGTTT 14211
64	Qy 45 IleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSerGluLeuLeuPhe 64
	US-10-001-254-6 (1-98) x AY186092 (1-33033)

MADO HIBAINAN ISAR

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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517
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(c) 1993 - 2004
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/geneseqn-embl/NA1983.DAT:*
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2250.748 Million cell updates/sec
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Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

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AAD40074
ID AAD40074;
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AC AAD40074;
XZ
AC AAD40074;
XX
BT 22-OCT-2002 (first entry)
XX
XX
DE Human IRAK4 DD (death domain) cDNA.
XX
Human; death domain; DD; death effe
XX
XX
Human; death domain; DD; death effe
XX
XX
Human; death domain; apoptosis; oncogenic
XX
XX
XX
Inflammation; allergy; autoimmunity
XX
immune-based pathology; fibrosis; a
XX
immune-based pathology; and immune-based pathology; and immune-based pathology; and immune-based pathology; fibrosis; a
XX
OS Homo sapiens.

ALIGNMENTS

Human; death domain; DD; death effector domain; DED; Chlamydia infection; NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy; gene; ss. Homo sapiens.

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The invention relates to an isolated polypeptide comprising a death CCC domain (DD), death effector domain (DED) or NB-ARC domain. The invention CC is useful for identifying a binding agent, preferably a protein or a drug CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or NIDD (NGFR-interacting Death Domain), with a candidate binding agent and CC detecting the association of the domain and the candidate binding agent, by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or CC chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and FPA. The invention is useful for modulating the CC level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and B cell CC immunoglobulin class switching, in particular apoptosis within a cell. CC immunoglobulin class switching, in particular apoptosis within a cell. CC cmuridarum, C. pneumoniae, and C. psittaci or a mucleic acid encoding the CC CTDD DD protein is useful for detecting a Chlamydia infection. The CC cmuridarum, C. pneumoniae, and C. psittaci or a mucleic acid encoding the CC constaing a pathology caused by the oncogenic proteins and for treating bacterial infections by modulating the activity of bacterial for directina infections by modulating the activity of bacterial allergy.
                    Query Match:
                                       Best Local Similarity:
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                                                                                                                   Alignment Scores:
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                                                                                                                                                                                             discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The proteir is useful for treating immune-based gathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense therapy and gene therapy. The present sequence is human IRAK4 DD cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases
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/note= "No start and stop codon"
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ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro

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Alignment Scores:

US-10-001-254-6 (1-98) x AAD40074

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                        AAA09310-20 are novel genes isolated by SEREX screening from a renal cancer cell line 1973/10.4. The genes encode cancer associated antigen precursors. These gene products are useful in methods for preventing, diagnosing and/or treating disorders, especially cancer, associated with abnormal expression of human cancer associated antigens. The method comprises contacting a sample from a subject with an agent that specifically binds to the nucleic acid molecule or expression product (or fragment) complexed with a human leukocyte antigen (HLA) molecule and determining the interaction between the agent and the nucleic acid molecule or the expression product as a determination of the disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cancer associated antigen precursor DNA, clone NY-REN-64.
 Sequence 833
                                                                                                                                                                               Claim 57; Page 85; 121pp; English
                                                                                                                                                                                                         preventing, diagnosing and/or treating disorders associated with abnormal expression of human cancer associated antigens
                                                                                                                                                                                                                                                  WPI; 2000-303774/26.
P-PSDB; AAY92347.
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05-OCT-1998;
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      IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro

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E, Chen Y,
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  226 T; 0 other;
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RESULT 3
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Best Local Similarity:
        New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other disease
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29-JUN-2001;
                                                                   WPI; 2002-500222/53.
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                                                                                                                                                                                                                                                                                                                                        NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; archritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy; gene; ds.
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2001US-301889P.
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                                                                                                                                                                                                                                                          /product= "Human IRAK4"
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RESULT 4
AAS76805
ID AAS7
XX
AC AAS7
XX
DT 13-F
XX
DE DNA
XX
DKW Huma

AAS76805

standard;

13-FEB-2002

(first entry)

DNA encoding novel human diagnostic protein #12609.

Human; chromosome mapping; gene mapping; gene therapy;

forensic;

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DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention CC is useful for identifying a binding agent, preferably a protein or a drug CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or CC detecting the association of the domain, with a candidate binding agent and CC detecting the association of the domain and the candidate binding agent and CC spectroscopy (MS) and FPA. The invention is useful for modulating the CC level of a cell process such as cell protein and B cell stress responses, responses to microbial infection and B cell cimmunoglobulin class switching, in particular apoptosis within a cell. CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the crimention is useful for modulating the activity of noncogenic proteins, CC for treating a pathology caused by the oncogenic proteins and for CC treating bacterial infections by modulating the activity of bacterial for CC discovery of drugs that suppress infection and other diseases. The protein cCC with cell division, inflammatory diseases such as sepsis, fibrosis, allergy, the protein inflammatory diseases such as sepsis, fibrosis, cCC with cell division, inflammatory diseases. The invention is used in antisense ccc therapy and gene therapy. The present sequence is human IRAK4 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ention relates to an isolated polypeptide comprising (DD), death effector domain (DED) or NB-ARC domain. 7
GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu
                                                                                                                                                                       AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer
                                                                                                                                                                                                                                              GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr
                                                                                                                                                                                                                                                                                              ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
                                                                           GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG
                                                                                                                                                  AATCAGTTTCACATAAGGAGTTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
                                                                                                                                                                                                                           ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
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                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, complymerase chain reaction (PCR) primers, oligomers, and for chromosome complymerase chain reaction (PCR) primers, oligomers, and for chromosome complymerase chain recombinant production of (II). The complymerase chain rescribed in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypucleotide sequences have applications in classifications in composible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and contains activity. ANS94564 represent novel human contains to assess biodiversity are the sequences of the invention.
                                                                                                                                                                                                                                                                      Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                         Sequence 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID No 12609; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
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                                                                                 GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr
                   AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
                                                               CAAGAAGGA
                                                                                                                                ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
                                                                                                                                                                  ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
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that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or NB-ARC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or NID6 (MGFR-interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent, by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NWR), mass spectroscopy (MS) and FPA. The invention is useful for modulating the stress responses such as cell proliferation, cell adhesion, cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specifically reactive with CTDD DD of C. trachomatis, C. muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the invention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reed JC, Godzi
Stenner-liewen
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29-JUN-2001; 2001US-301889P
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                                                                                                                                                                                                                                                                                                           chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rininitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; inflammatory bowel disease; gour; Crohn's disease; ulcerative colitis; Behcet's syndrome; ankylosing spondylltis; IL-1 receptor/Toll receptor; sarcoidosis; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               II.; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD;
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                                                                                                                                                       Location/Qualifiers
1..1383
                                                                                        /*tag= a
/product= "Human IRAK-4'
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Conservative:
Mismatches:
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GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu

80 204 60 144 40 84

AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspAspArgTyr ACATATGTGCGCTGAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT

AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT

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                                                               US-10-001-254-6 (1-98) x AAD10197 (1-1383)
                                                                                                                                         Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                Score:
                                                                                                                                                                                                                                      Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                   CC or allergic rhinitis), transplant rejection, autoimmune diseases (e.g., crheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis (C or diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma), (CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases (e.g., stroke and atherosclerosis), diseases (cof the central nervous system (e.g., neurodegenerative disease), CD14 (cc mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis, CC psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic dermatitis), inflammatory bowel disease (e.g., Crohn's disease and culturative colitis), Behcet's syndrome, ankylosing spondylitis, gout, (corrative colitis), Behcet's syndrome, ankylosing spondylitis, gout, (corroldosis and ophthalmic diseases and conditions. The inhibitors of CC IRAK-4 activity or expression are used to inhibit signal transduction cresulting from the activation of an interleukin-1 receptor (II-IR)/Toll (crecaptor in a cell. They also inhibit the activation of a transcription (create and conditions are used to resting the function of create and conditions are used to resting the function of create and conditions and conditions and for the development of potential treatments (corrates and conditions and for the development of potential treatments of create and conditions and in correct the activations. IRAK-4 sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated kinase (IRAK)-4. IRAK associate with activated IL-1, IL-18 and other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)-kappaB activation. The IRAK-4 inhibitors are useful for treating inflammatory diseases such as pulmonary diseases and diseases of the airway (e.g., adult respiratory disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD), pulmonary fibrosis, interstitial lung disease, asthma, chronic cough pulmonary fibrosis, interstitial lung disease, asthma, chronic cough
                                                                                                                                                                                                                                                                                                        Sequence 1383 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating asthma, allergic rhinitis, multiple sclerosis and skin cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Fig 2; 89pp; English.
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                                                                                                                                                                                                                                                                                                                                                         also used
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ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is a cDNA encoding human interleukin (IL)-1 receptor kinase (IRAK)-4. IRAK associate with activated IL-1, IL-18
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                                                                                                                                                            Length:
Matches:
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inhibitors are useful for treating inflammatory diseases such as pulmonary diseases and diseases of the airway (e.g., adult respiratory disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD), pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or allergic rhinitis), transplant rejection, autoimmune diseases (e.g., rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis or diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma), cardiovascular diseases (e.g., stroke and atherosclerosis), diseases of the central nervous system (e.g., neurodegenerative disease), CD14 mediated sepsis, osteoarthritis, osteoporosis
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                                                                                                                                                                                      The present sequence is a cDNA encoding mouse interleukin (II)-1 receptor associated kinase (IRAK)-4. IRAK associate with activated II-1, II-18 and other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)-kappaB activation. The IRAK-4
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                                                                                                                                                                                                                                                                                                                                             Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating gout, asthma, allergic rhinitis, multiple sclerosis and skin cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wesche H,
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)B; AAE05399.
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                                                                                                                                                                                                                                                                                                            26; Fig 4; 89pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                    11-APR-2000;
21-JUN-2000;
01-SEP-2000;
05-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local S
y Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        are also used in gene therapy and in antisense therapy.
                                                                                                                                                                                                                                                                                                                WO200177168-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytostatic; antitumour; lung small cell cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lung small cell carcinoma antigen, cDNA #149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS61608 standard;
                                                                                                                                                                                                11-APR-2001; 2001WO-US11859.
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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; 2000US-229763P.
; 2000US-230629P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc polynucleotides (I) and polypeptides (II) used in a method of detecting cancer in a patient. The method is optionally performed by utilising oligonucleotides (III), where the biological sample cc from the patient is contacted with (III), detecting the amount of polynucleotide hybridised to (III) in the sample and comparing the amount of polynucleotide to a predetermined cut-off value and thereby determining cancer in a patient. (I), (II) or antigen-presenting cells expressing (II) is useful for stimulating and/or expanding T cells expecific for a tumour protein. The method comprises contacting T cells with one of the components under conditions to permit the stimulation and/or expansion of the cells. A composition comprising (I) is useful for stimulating an immune response in a patient and for inhibiting the cells isolated T cell population is useful for removing tumour cells from the biological sample and for inhibiting the development of cancer in a patient. AAS61460-AAS61874 represent novel human lung small cell cancer antigen coding seminates of the invention.
DNA encoding novel human diagnostic protein #12607.
                                13-FEB-2002
                                                               AAS76803;
                                                                                            AAS76803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 501 BP;
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                                                                                                                                                                                                                  TTGAATACTGTTTGACTGGGGGCACCACAATTGGACAGTTGGTGATCTTGTGGATCTTT
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                             (first entry)
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lung cancer -
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                               polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques CC for restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in CC diagnostics, forensics, gene mapping, dentification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC and to produce other types of data and products dependent on DNA and CC and occording sequences of the invention.

CC Septiment of the however this patent did not appear in the printed as pecification, but was obtained in electronic format directly from WIPO as for which in the hombing the products or the printed of the products of the invention.
                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutatio responsible for genetic disorders or other traits and to assess
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                       174
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2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relates to isolated polynucleotide (I) and II) sequences. (I) is useful as hybridisation probes,
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RESULT 10
AAD40084
The invention relates to an isolated polypeptide comprising a death chomain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED or NIB-ARC domain in from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or NIB-ARC domain in the candidate binding agent and detecting the association of the domain and the candidate binding agent, by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NNA), mass spectroscopy (MS) and FPA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specifically reactive with CTDD DD GC. trachomatis, C. muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the invention is useful for modulating the activity of correction. The
           invention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for treating bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The proteins useful for treating immune-based pathologies, pathologies associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation allergy, sepsis, autoimmunity, allograft rejection and other diseas
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29-JUN-2001; 2001US-301889P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD40084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 19; Page 195; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-500222/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              death do
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Godzik A,
iewen F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Human IRAK4 short protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pawlowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
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Roth W;

inflammation, other diseases

for treating immune-based pathologies division, inflammatory diseases such

protein

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RESULT 11
AAS76802
ID 76802
ID AAS76
XX AAS76
XX DA 6
XX DA 6
XX Humar
XX Homo
XX CHain
XX Homo
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Query Match:
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, us diagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arthritis, graft versus host disease. therapy and gene therapy. The present
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73.
P-PSDB; ABG12615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding
                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                 biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                1; SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AsnGlnPheHisIleArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
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2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
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                                                                                                                                                                                                                                  No 12606; 103pp;
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47.78$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y
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                                                                                                                                                                                                                                  English
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to assess
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Best Local Similarity:
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                                                                                                                                       29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
 Primer sets for synthesizing full-length cDNAs defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                       WPI; 2001-318749/34.
                                                                                                                                                                                                     28-JUL-2000;
                                                                                                                                                                                                                               07-FEB-2001.
                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                      Human; primer;
                                                                                                                                                                                                                                                                                                                               Human cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                   AAH13798;
                                                                                                   (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                         26-JUN-2001
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                                                             Isogai T,
, Sugiyama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AsnGlnPheHisIleArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACATATGTGCGCTCCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
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                                                                                                                           99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                      2000EP-0116126.
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                                                                                                                                                                                                                                                                                                  detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                             99JP-0248036.
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247.00
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                                                             Nishikawa T,
T, Wakamatsu
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polynucleotides, particularly the 5602 the specification, and for the detection
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                                                             Hayashi K,
A, Nagai I
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Matches:
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                                                             Saito K,
Otsuki
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                                                             Yamamoto T;
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##X#X55555555555555555555555555555555
                                  CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC complementary strand of a polynucleotide which comprises a 5'-end
CC oligonucleotide which comprises a 3'-end sequence complementary to a
CC polynucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primers sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH35893 represent human amino acid sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
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US-10-001-254-6 (1-98) x AAH13798 Query Match: Best Local Percent Similarity: No.: 775 Similarity: ۳ 1.5e-24 247.00 100.00% 100.00% 47.78% (1-2213)Length: Matches: Conservative: Mismatches: Gaps: Indels: 0000 2213 46

Sequence 2213

BP;

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ABQ56733 standard; cDNA;
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                                                                AsnGlnPheHisIleArg
                                                                                               GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr
                                                                                                                                 ACATATGTGCGCTGCATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
                                                                                                                                            ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
                                          AATCAGTTTCACATAAGA
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RESULT 13
ABQ56733
ID ABQ56 Human; colon cancer; cancer; tissue profiling; forensic; mapping; genetic analysis; diagnostic; antisense therapy; gene; ss. Human 02-OCT-2001; 2001WO-US30732 11-APR-2002. Homo sapiens 02-AUG-2002 ABQ56733; colon cancer related nucleotide sequence SEQ ID NO:428 (first entry)

XXCCCCCCCCCCCCXXXXTTTXXXXIII

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RESULT 14
AAF44695
ID AAF44
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AC AAF44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed in cancer tissues. ABB78993 to ABB79004 represent proteins cencoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and for detecting the presence or absence of a polynucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) and for determining the phenotype of cells in a sample of cells from a patient. (I) is useful for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity:
Novel protein kinase cDNA, SEQ ID
                                               27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 796pp; English.
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                                                                                                                                               AAF44695 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid that is differentially expressed in cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-OCT-2000; 2000US-237271P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 GlyLeuIleArgLysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAla
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                                                                                                                                                                                                                                                                                                                                         GGCACCACAAATTGCACAGNTGGGGGATCTTGTGNATNCCNCGAANCACAACNGAATTTN
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                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                           Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a novel protein kinase. The nucleic acids and the protein kinases they encode may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase entragonists may also be used to down regulate kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, cardiomyopathies, strokes, renal failure, oxidative stress related disorders, chronic inflammatory bowel disease, oxidative stress related disorders, chronic inflammatory bowel disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dematological; antiidiabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                             Sequence 1791
                                                                                                                                                                                                                                                                                                                                                                                                             chronic inflammatory pelvic disease, multiple sclerosis, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 2; 310pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding kinase polypeptides, use treating immune-related diseases and disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAB65667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plowman GD, Martinez
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                                                                                                                                                                                                                                                                                                                                                                                            reproductive disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurodegenerative diseases and/or cancers -
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                            48 PheGluAlaLeuLeuGlnThrGlyLysSerProThrSerGluLeuLeuPheAspTrpGly 67
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ATTGAAAAGTATGTAGACCAAGGTAAAAGTGGAACAAGAGAATTACTTTGGTCCTGGGCA
                                                                                             AlaValAlaIleLysLysProSerGlyAspAspArgTyrAsnGlnPheHisIleArgArg
                                                                                                                                                              ValGlyLeuIleArgLysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeu 27
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Query Match:
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AAC84459
                                                                                   Pred. No.:
                                                                                                Alignment Scores:
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                                                                                                                                                      The invention provides interleukin-1 receptor associated kinase-3 (IRAK3) proteins. The IRAK3 proteins are useful in drug screening, particularly for screening modulators of IRAK3. The modulator is useful for treating a disease or condition associated with interleukin-1 (II-1) family activity. It may also be used for manufacturing a medicament for the treatment of these diseases or conditions which include inflammations, post-operative septicemia autoimmune diseases (e.g. Crohn's disease, psoriasis, multiple sclerosis, transplant rejection or graft versus host disease) stroke, ischemia, reperfusion injury, acute respiratory disease syndrome, restenosis, atherosclerosis, AIDS (acquired immune deficiency syndrome), bone diseases (e.g. osteoporosis), cancer, Alzheimer's disease, rheumatoid arthritis, poor wound healing or asthma. The present sequence represents an IRAK3 protein encoding cDNA.
                                                                                                                             Sequence 2277 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRAK3; interleukin-1 receptor associated kinase-3; drug screening; interleukin-1; IL-1; antiinflammatory; cytostatic; immunomodulator; immunosuppressive; vulnerary; anti-human immunodeficiency virus; HIV; nootropic; neuroprotective; antiarthritic; antiasthmatic; respiratory; osteopathic; vasotropic; antiarteriosclerotic; cerebroprotective; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                      Interleukin-1 receptor associated kinases, useful for screening drugs for treating diseases affected by interleukin-1 activity, e.g. inflammations or autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-071072/08.
P-PSDB; AAB48173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 22-24; 26pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUN-1999;
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             Matches:
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US-10-001-254-6 (1-98) x AAC84459 (1-2277)

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233	68	173	48	134	28	74	
233 CAGAAAAACAAGACCATCGGTGACCTTTTACAGGTCCTC 271	ThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80	173 ATTGANAAGTATGTAGACCAAGGTAAAAGTGGAACAAGAGAATTACTTTGGTCCTGGGCA 232	48 PheGluAlaLeuLeuGlnThrGlyLysSerProThrSerGluLeuLeuPheAspTrpGly 67	134 GCAGAGAGACTTTCAAGC172	28 AlaValAlaIleLysLysProSerGlyAspAspArgTyrAsnGlnPheHisIleArgArg 47	74 CTCGGAGAGCTCTGCGCTGTTCTGGACAGCTGCGACGGCGCGCGC	PheIleAspProGlnGlu

Search completed: January 18, Job time: 120.536 secs 2004, 01:31:59 BEST AVAILABLE COPY

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Result
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-Q=(cgn2 1)(USPT0_spool)(USI0001254/runat 16012004 152426 19815/app_query.fasta_1.1109
-DB=Published_Applications_NA_QFMT=fastap_SUFFIX=rnpb-_MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits_-START=1 -ERUN=-1 -MATRIX=biosum62
-TRANS=human40.cdi_-LIST=45 -DOCALIGN=200 -THR_SCORE=pct_-THR_MX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto_-NORM=ext_-HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10001254_@CGN_1 1_534_@runat_16012004_152436_19815
-NCPU=6 -ICPU=3 -NO_MMAP_-LARGEQUERY_-NEG_SCORES=0 -WAIT_-DSPBLOCK=100
-LONGLOG_-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPDEXT=0.5
-FGAPDP=6 -FGAPEXT=7 -YGAPDP=10--YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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-MODEL=frame+_p2n.model -DEV=xlh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
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                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
Query
Score Match Length DB
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517
1 TYVRCLNVGLIRKLSDFIDP.....LLIQNEFFAPASLLLEDAVP
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                         /cgn2_6/pcodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/pcodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US06
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_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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Sequence 5618, Ap	TA '61 A	oquetice 40,	Seguence 49	equence 49.	quence 49,	e 19,	e 141	equence 141792	equence	quence 10114,	e 286,	equence 288	equence 1, Ap	e 13:	equence 137	equence 72568,	e 72567,	equence 72568,	72567,	e 50724,	equence 50723,	equence 50724,	equence 50723	equence	equence 709, 1	3590,	equence 3587,	Sequence 3589,	14	equence 3,	equence 1, Appli	equence 1	1430 4	equence 3,	quence 1	e 25	e 10,	quence 149,	e 4,	equence 2,	equence 27,	e 3, 2	equence 15, Ap	Sequence 5, Appli	

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ALIGNMENTS

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US-10-001-254-5

| Sequence 5, Application US/10001254
| Publication No. US20030049702A1
| GENERAL INFORMATION:
| APPLICANT: Reed, John C.
| APPLICANT: Reed, John C.
| APPLICANT: Fiorentino, Loredana
| APPLICANT: Fiorentino, Loredana
| APPLICANT: Roth, Wilfred
| APPLICANT: Roth, Wilfred
| APPLICANT: Roth, Wilfred
| APPLICANT: Stenner-Liewen, Frank
| TITLE OF INVENTION: NO. US20030049702A1el Death Domain Proteins
| FILE REFERENCE: P-LJ 5037
| CURRENT FILING DATE: 2001-11-15
| PRIOR APPLICATION NUMBER: 60/301,889
| PRIOR APPLICATION NUMBER: 60/301,889
| PRIOR APPLICATION NUMBER: 60/301,889
| PRIOR FILING DATE: 2000-11-17
| NUMBER OF SEQ ID NOS: 62
| SEQ ID NOS: 62
| SEQ ID NOS: 62
| LENGTH: 294
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GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
APPLICANT: Godzik, Adam
APPLICANT: Fiorentino, Loredana
APPLICANT: Fiorentino, Loredana
APPLICANT: Fiorentino, Loredana
APPLICANT: Fiorentino, Loredana
APPLICANT: Roth, Wilfred
CURRENT: FILE NEWENTION: NO. US20030049702A1el Death Domain Proteins
FILE REFERENCE: P-LJ 5037
CURRENT FILING DATE: 2001-11-15
PRIOR PILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 1383
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1380)
US-10-001-254-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA;
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS;
; LOCATION: (1)...(294)
US-10-001-254-5
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Best Local Similarity:
Query Match:
 Score:
Percent Similarity:
Best Local Similarity:
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US-10-001-254-15
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                                                     Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/10001254
Publication No. US20030049702A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GAATTACTGTTTGACTGGGGCACCACAATTGCACAGTTGGTGATCTTGTGGATCTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 AsinGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
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 Length:
Matches:
Conservative:
Mismatches:
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Qy	B Q	D Qy	D Qy	Qy	US-10-00	Alignment: Pred. No:: Score: Percent Si Best Local Query Matcl	RESULT 3 US-09-966-451- SEQUENCE 3, PUDITCATION GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT FILE REFERE CURRENT APP CURRENT APP CURRENT FILE NUMBER OF S SEQ ID NO 3 SEQ ID NO 3 LENGTH: 28 TYPE: DNA ORGANISM: PRATURE: NAME/KEY: LOCATION: US-09-966-451-	B Q	Qy Db	Qy Db	D Qy	Qy .	US-10-001-	Query Ma DB:
81 IleGlnAsnG	61 GluLeuLeuP 254 GAATTACTGT	41 AsnGlnPheH 194 AATCAGTTTC	21 GlnGluGlyT 134 CAAGAAGGAT	1 ThrTyrValA 74 ACATATGTGC	0-001-254-6 (1-98) x	Scores: milarity: Similarity:	SSULT 3 :09-966-451-3 :09-966-451-3 :09-966-451-3 sequence 3, Application US/0996 Publication No. US20030087856A1 GENERAL INFORMATION: APPLICANT: C. Frank Bennett APPLICANT: SUBAN M. Freier TITLE OF INVENTION: ANTISENSE FILE REFERENCE: FTS-03-4 CURRENT APPLICATION NUMBER: US CURRENT APPLICATION NUMBER: US CURRENT FILING DATE: 2001-09- NUMBER OF SEQ ID NOS: 88 SEQ ID NO 3 LENGTH: 2817 TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: CDS LOCATION: (50)(1432) :-09-966-451-3	81 IleGlnAsnG 265 ATCCAAAATG	61 GluLeuLeuP 205 GAATTACTGT	41 AsnGlnPheH 145 AATCAGTTTC	21 GlnGluGlyTrp 85 CAAGAAGGATGG	1 ThrTyrValA 25 ACATATGTGC	1-254-6 (1-98) x	Match:
eGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro	heAspTrpGlyThrTl TTGACTGGGGCACCAC	isIleArgArgPheGl acataaggagatttg <i>j</i>	rpLysLysLeuAlaVa GGAAGAAGTTAGCTGT	rgCysLeuAsnValGl CTGCCTCAATGTTGC	US-09-966-451-3	5.01e-71 I 517.00 N 100.00% O 100.00% N	Application US/09966451 No. US20030087856A1 RMATION: C. Frank Bennett Susan M. Freier VENTION: ANTISENSE MODULATION NCE: RTS-0324 LICATION NUMBER: US/09/966,45: LING DATE: 2001-09-28 EQ ID NOS: 88 LI7 Homo sapiens CDS CDS (50) (1432)	IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro	heAspTrpGlyThrTh 	isIleArgArgPheGl 	LysLysLeuA AAGAAGTTAG	rgCysLeuAsnValG] CTGCCTCAATGTTGG	US-10-001-254-15	100.00% I
laSerLeuLeuLeuP	nrAsnCysThrValG CAAATTGCACAGTTG	luAlaLeuLeuGlnT AGCATTACTTCAAA	alAlaIleLysLysP AGCTATTAAAAAAC	lyLeuIleArgLysL ACTAATTAGGAAGC	3 (1-2817)	Length: Matches: Conservative: Mismatches: Indels: Gaps:	OF IL-1	laSerLeuLeuLeuP GAGTCTTTTGCTCC	nrAsnCysThrValG DAAATTGCACAGTTG	uAlaLeuLeuGlnT AGCATTACTTCAAA	alalaileLysLysP ragctattaaaaaac	lyLeuIleArgLysL ACTAATTAGGAAGC	15 (1-1383)	Indels: Gaps:
roAspAlaValPro 98	GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80 	AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60 	GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspAspArgTyr 40 	ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20 		2817 98 0	RECEPTOR-ASSOCIATED KINASE-4	roAspAlaValPro 98 CAGATGCTGTTCCC 318	GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80 	AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60 	TrplyslysleuAlaValAlaIleLyslysProSerGlyAspAspArgTyr 40 	TValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20 		
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US-09-759-595-2
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; LOCATION: (50)...(1429)
US-10-001-254-27
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                    Sequence 2, Application US/09759595
Publication No. US20030059916A1
GENERAL INFORMATION:
APPLICANT: Wesche, Holger
APPLICANT: Li, Shyun
APPLICANT: Tularik Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 27
LENGTH: 2817
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Publication No.
APPLICANT: Li, Shyun
APPLICANT: Tularik Inc.
TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
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SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapien
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CANT: Lee, Sug Hyung
CANT: Roth, Wilfred
CANT: Stenner-Liewen, Frank
OF INVENTION: No. US20030049702A1el Death Domain Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION
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No. US20030049702A1
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Matches:
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Indels:
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; IOCATION: (1)..(1383)
; OTHER INFORMATION: human IRAK-4
US-09-759-595-2
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Query Match:
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Pred. No.:
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                                                                                                               SEQ ID NO 4
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SEQ ID NO 2
LENGTH: 1383
                                                                                                                                                 APPLICANT: Wesche, Holger
APPLICANT: Li, Shyun
APPLICANT: Tularik Inc.
PITTLE OF INVENTION: IRAK-4: Compositions and Methods of Use
FILE REFERENCE: 018781-003910US
CURRENT APPLICATION NUMBER: US/09/759,595
CURRENT FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US/01/76,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
                                 LENGTH: 1542
TYPE: DNA
ORGANISM: MUS SP.
FEATURE:
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CURRENT FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1
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OTHER INFORMATION: OTHER INFORMATION:
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513.00
98.98%
98.98%
99.23%
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                 IL-1 receptor-associated kinase
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Matches:
Conservative:
Mismatches:
Indels:
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; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE;
; NAME/KEY: misc_feature
; LOCATION: (1)...(501)
; OTHER INFORMATION: n = A,T,C or
US-09-833-790-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (163)..(15
; OTHER INFORMATION: 1
US-09-759-595-4
                                          Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-001-254-6 (1-98) x US-09-833-790-149 (1-501)
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 149
LENGTH: 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                         APPLICANT: Mohamath, Raodoh
APPLICANT: Indirias, Carol Y.
APPLICANT: Indirias, Carol Y.
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tongtong
APPLICANT: Secrist, Heather
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                                          Conservative: Mismatches: Indels:
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Matches:
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Query Match:
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US-10-001-254-25
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Publication No. US20030087856A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
FILE REFERENCE: RTS-0324
                                                                                                   Sequence 25, Application US/10001254
Publication No. US20030049702A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/966,451
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 10
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Fiorentino, Loredana
APPLICANT: Lee, Sug Hyung
APPLICANT: Roth, Wilfred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 AATCAAGTTTCACATAAGGAGATTTGAAGCATT-CTTCAAACTGGAAAAAGTCCCACTTC 223
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                                                                                                                                                                                                                  PhePheAlaProAlaSerLeuLeuLeuPro 94
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Patent No. US20020049300A1
GENERAL INFORMATION:
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and Methods
FILE REFERENCE: T98-019
CURRENT APPLICATION NUMBER: US/09/863,549
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: 09/135,232
PRIOR APPLICATION NUMBER: 09/135,232
PRIOR FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 25
LENGTH: 211
                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1
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TITLE OF INVENTION: No. US20030049702Aiel Death Domain Proteins
FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
CURRENT FILING DATE: 2001-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/301,889 PRIOR FILING DATE: 2001-06-29
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NAME/KEY: CDS
LOCATION: (1)...(177)
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ORGANISM: Homo
                                                                                                                                        NAME/KEY: CDS
LOCATION: (64)
                                                                                                                                                                        FEATURE:
                                                                                                                                                                                  ORGANISM: human
                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                   ENGTH:
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CURRENT APPLICATION NUMBER: US/10/098,841

CURRENT FILING DATE: 2002-03-13

PRIOR APPLICATION NUMBER: 09/598,042

PRIOR FILING DATE: 2000-06-20

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR PRIOR PRIOR DATE: 2000-01-21

PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 3000-01-21

NUMBER OF SEQ ID NOS: 331
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                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Tom
APPLICANT: Zhang, Jie
APPLICANT: Qian, Xiaohong B.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20020197679A1el Nucleic
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                                LENGTH: 22
TYPE: DNA
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                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens FEATURE:
NAME/KEY: CDS
LOCATION: (7)..(1806)
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8 ValGlyLeuIleArgLysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeu
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Zhao, Qing A.
Ren, Feiyan
Chen, Rui-hong
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Ma, Yunqing
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US-10-340-545-1
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                                                                                                                                                                         Sequence 1432, Application US/10198846 Publication No. US20030099974A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1
LENGTH: 1888
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: IRAK-M IS A NEGATIVE REGULATOR OF TOLL-LIKE RECEPTOR SIGNALING FILE REFERENCE: YU-P01-011
CURRENT APPLICATION NUMBER: US/10/340,545
CURRENT FILING DATE: 2003-01-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/348176
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 28
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ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                        GCACAGAAAACAAAACGATCGGCGACCTTTTAGAGGTTCTC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCTGGGAGAGCTTTGCGGGATCCTGGACAGCTGGGATGGCCCCGCTCGGCTGGTGGGGC
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                                                                                                                                                                                                                                                                                                                                              GlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
                                                                                                                                                                                                                                                                                                                                                                                          CATATTGAAAAGTACCTAAAACCAAGGTAAAAGTGGAACAAGAGAATTGCTCTGGTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSerGluLeuLeuPheAspTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGCGGAGCGACTTTCAAAC-------AGCTGGCTGGATGTTCGT
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95.00
48.65%
32.43%
18.38%
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Indels:
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                                              PREVENTION,
                                                                     AND METHODS
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                                                                                  CURRENT APPLICATION NUMBER: US/10/366,288
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: 60/357,391
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 60/380,249
PRIOR FILING DATE: 2002-05-13
PRIOR FILING DATE: 2002-05-13
PRIOR PPLICATION NUMBER: 60/391,306
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: 60/406,297
PRIOR FILING DATE: 2002-08-27
PRIOR FILING DATE: 2002-08-27
PRIOR FILING DATE: 2002-08-27
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LENGTH: 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/103
Publication No. US20030216288A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
  PRIOR APPLICATION NUMBER: 60/412,007
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: 60/417,508
PRIOR FILING DATE: 2002-10-10
                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: AIDS AND HIV-RELATED DISORDERS USING 1414, 1481, 1553, TITLE OF INVENTION: 34021, 1720, 1683, 1552, 1682, 1675, 18825, 9952, 5816 TITLE OF INVENTION: 10002, 1611, 1371, 14324, 126, 270, 312, 167, 326, 189 TITLE OF INVENTION: 6747, 1793, 1784 OR 2045 MOLECULES FILE REFERENCE: MPIO2-025FIRNOWNIM
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Powell, Douglas
APPLICANT: Weich, Nadine S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: AIDS AND HIV-RELATED DISORDERS USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: 2, 7, 217
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; SOFTWARE: FASTSEQ for Wi
; SEQ ID NO 19
; LENGTH: 1782
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-366-288-19
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Query Match:
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US-09-773-753-1
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PRIOR FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 52
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20005-3934
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk
CURRENT APPLICATION NUMBER: US/09/773,753
PLING DATE: 02-Peb-2001
CLASSIFICATION COMP
           NAME: STEFFE, ERIC K.

RECISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.1010000/EKS/AJK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/980,060

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HUMAN IRAK-2 NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NI, JIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 TGGTGGTGGGGCATGCCGCAGGCACCGTCCAGCAACTTGTGGACCTCCTGTGCCGCCTG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 CCCATTCCAGCCTTCCCTGACTCTGTG 339
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TELEFAX: (202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUZIO, MARTA
DIXIT, VISHVA M.
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NAME/KEY: CDS
LOCATION: 34..1803
SEQUENCE DESCRIPTION: SEQ ID
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1806 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
337 CCCATTCCAGCCTTCCCTGACTCTGTG
                                                         277 GAGCTCTACCGGGCTGCCCAGATCATCCTGAACTGGAAACCGGCTCCTGAAATCAGGTGT 336
                                                                                                              217 TGGTGGTGGGGCATGCGGCAGGCCACCGTCCAGCAACTTGTGGACCTCCTGTGCCGCCTG
                                                                                                                                                                      157 CTGCGGAAGATCAAGTCCATGGAGCGGGTGCAGGGTGTGAGCATCACGCGGGAGCTGCTG
                             94
                                                                                    84 GluPhePheAlaProAlaSerLeuLeuLeu---
                                                                                                                                       64 PheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeuIleGlnAsn 83
                                                                                                                                                                                        TYPE: nucleic acid STRANDEDNESS: double
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31.88%
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                            ProAspAlaVal 97
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Matches:
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Indels:
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Search completed: January 18, Job time: 153.603 secs 2004, 09:05:28

> 93 276

216 63 BEST AVAILABLE COPY

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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_/USPTO_spool/US10001254/runat 16012004 152424 19723/app_query.fasta_1.1109
-Q=/cgn2_P/USPTO_spool/US10001254/runat 16012004 152424 19723/app_query.fasta_1.1109
-DB=EST -OFMT=fastap -SUFFIX=ret -MIMMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR MIN=0 -ALICN=15 -MODE=LOCAL
-UNITSTED -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=2000000000
-USER=US10001254 @CGN 1 1 4382 @runat 16012004 152424 19723 -NOPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XCAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Fgapop 6.0 , F
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January 18, 2004, 01:11:43; Search time 956.969 Seconds (without alignments) 2488.940 Million cell updates/sec
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              em_gss_hum:
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

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ALIGNMENTS

REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	BG164491	RESULT 1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 859)	Homo sapiens	Homo sapiens (human)	EST.	BG164491.1 GI:12671194	BG164491	mRNA sequence.	ens cDNA c	BG164491 859 bp mRNA linear EST 06-FEB-2001		

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RESULT 2
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TITLE
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                                       ORGANISM
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
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Tissue Procurement: ATCC
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National Institutes of Health, N
Unpublished
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                     Homo sapiens
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                                                                                                                             mRNA sequence.
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                                                                                              BG616438.1 GI:13667809
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                                                      Homo sapiens (human)
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/lab_host="NHH0B (phage-resistant)"
/clone_lib="NIH_MGC_89"
/clone_tib="NIH_MGC_89"
/note="forgan: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 168 c 190 g 235 t
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/db_xref="taxon:9606"
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: ATCC
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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/lab host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_61"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
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EST.
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Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
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Analysis of bovine mammary gland EST
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Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P., Connor, E.B. Cho.J.. Sultana, R., Shade, L., Wray, J.E., Wells, K.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos.
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                                                                                      AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
                                                                                                                                       GAGTTACTGTTTGACTGGGGCACCACAATTGCACAGTTGGTGATCTTGTGGATATTTTG
                         GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu 80
                                                                                                                                                                                                                            ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
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n. Genome 13 (7), 373-379 (2002)
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/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sall;
/ibrary made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
8 8 9 105 t
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/lab_host="DH10B"
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|mol_type="mRNA"
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41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer
                                                                21 GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr
                                                                                                                            92 ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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602130160F1 NIH_MGC_56 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCCAAAATGAGTTTTTTGCCCCCTGCAAGTCTTTTGCTACCAGATGCTGTACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/clone_llb="NIH_MGC_56"
/clone_llb="NIH_MGC_56"
/clone_llb="NIH_MGC_56"
/site_2: Sfil (Glontech); Site_1:
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
/site_2: Sfil (ggccattatggcc);
Stale_2: Sfil (ggccattatggcc);
And 3: adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTGAAGGCCGAAGCGCCACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

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/db_xref="taxon:9606"
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, t
Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0272 row: B column: 01
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503 bp mRNA linear EST 19-NOV-2002 (20272801-5N NIA Mouse 7.5-dpc Whole Embryo CDNA Library (Long) Mus musculus cDNA clone NIA:CO272B01 IMAGE:30017484 5', mRNA sequence.
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Contact: Dawood B. Dud
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Systematic Analyses of NIA Mouse 7.5-dpc Whole Embryo cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATCCAAAATGAATTTGTTGGCTCCTGCAAGTCTTTTGCTCCCAGATGCTGTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 503)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 503
/tissue_type="whole embryo including extraembryonic
tissues at 7.5-days postcoitum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                    /clone_lib="NIA Mouse 7.5-dpc Whole Embryo cDNA Library
(Long)"
                                                                                                                                                                                                                                                                                 (Long)
                                                                                                                                                                                                                                                                                                                                                                 clone="NIA:C0272801 IMAGE:30017484"
                                                                                                                                                                                                                                                                                                                                                                              db_xref="niaEST:C0272B01-5N"/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                                                                                                                                           dev_stage="7.5-days postcoitum"
lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                         strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAACTGCTGTTTGACTGGGGCACCACGAACTGCACAGTTGGCGACCTTGTGGATCTACTG
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431

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US-10-001-254-6 (1-98) x CA538859 (1-503)
                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                          252 CAAGAAGGGTGGAAGAAATTAGCAGTAGCTATCAAAAAAGCCGTCCGGCGACGACAGATAC
GluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeu
                                                                       AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
                                                                                                                                             GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr
                                                                                                                                                                                                ACATACATACGCAACCTTAATGTGGGGATCCTTAGGAAGCTGTCGGATTTTATTGATCCT
                                                   AATCAGTTCCATATAAGGAGATTCGAAGCCTTACTTCAGACCGGGAAGAGCCCCCACCTGT
                                                                                                                                                                                                                     ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed by Yulan Piao (NIA)."

146 c 138 g 100 t
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476.00
95.92%
90.82%
92.07%
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Indels:
Gaps:
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0 0
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                 80
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                                                      371
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Contact: Yong Qian
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
Plate: H4014 row: C column: 09
Seg primer: -21M13 Reverse VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter P.R., Stagg, C.A., Bassey, U., Aiba, K., Hamatani, T., Luo, A.G., Kelso, J., Hide, W. and Ko, M.S.H. Assembly, verification, and initial annotation of NI BQ552228 598 bp H4014C09-5 NIA Mouse 7.4K cDNA BQ552228 BQ552228.1 Genome Res. cDNA clone set Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mus musculus Mus musculus (house mouse) H4014C09 5', mRNA sequence. 22354164 12466305 quality sequence stop: 598 Location/Qualifiers /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6" GI:21453114 12 (12), 1999-2003 (2002) ģ Clone Set Mus musculus linear Carter, M.G., Kargul, G.J., EST 20-JUN-2002 7.4K mouse cDNA clone Martin

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REFERENCE
AUTHORS
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BB660378
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Best Local Similarity:
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                                                                                                                                                                                                     1 (bases 1 to 610)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shinagata, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                      1-7-22 Suehiro-cho, Tsurumi-ku, Tel: 81-45-503-9222
                                                                                                                                                 Unpublished
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB660378 RIKEN full-length enriched, 13 musculus cDNA clone D430042L21 5', mRNA
                                                                                                                                                                                       RIKEN Mouse ESTs (Arakawa, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCCAGATTGAGCTGTTTGCCCCCCGCCACTCTCCTGCTGCCGGATGCCGTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAlaValPro 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGAAGGGTGGAAGAATTAGCAGTAGCTATCAAAAAAGCCGTCCGGCGACGACAGATAC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATCAGTTCCATATAAGGAĞATTCGAAGCCTTACTTCAGACCGGGAAGAGCCCCACCTGT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACATACATACGCAACCTTAATGTGGGGATCCTTAGGAAGCTGTCGGATTTTATTGATCCT 235
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                      81-45-503-9216
genome-res@gsc.riken.go.jp,
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/note="Vector: pspORT1; Site_1: SalI; Site_2: NotI; This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."
174 c 163 g 111 t
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/lab_host="DH10B"
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/clone="H4014C09"
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/db_xref="taxon:10090"
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US-10-001-254-6 (1-98) x BB660378 (1-610)
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21 GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr
                                                                                   1 ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
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wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) KOndo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizav,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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    Y. and Hayashizaki, Y

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RIKEN full-length enriched, 13 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="lung"
/dev_stage="13 days embryo"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Arakawa,T., Carninci, P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A, Arakawa,T., Carninci,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Koud., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Koud., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasak,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabb,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN, Mouse ESTs (Arakawa,T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB613447.1 GI:16454055
EST.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKEN integrated sequence analysis (RISA) system--384-form sequencing pipeline with 384 multicapillary sequencer. Genc 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Y. and Hayashizaki,Y.
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Tel: 81-45-503-9222
                                                                                                                                                                             further details.
e mouse tissues
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with uman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computer-based methods for the mouse full-length cDNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 638)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,I
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BY721552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization
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/dev_stage="10 days neonate"
/lab_host="DH10B"
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Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
Quackenbush,J., Schriml,L.M., Kanappin,A., Matsuda,H., Batalov,S.,
Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani
L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest
A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A.,
Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J.,
Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M.,
King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons
P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki
H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D.,
Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J.J., Ring
B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou
M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale
R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y.,
Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A.,
Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura
M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii
Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata
K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander
R.S., Rogers,J., Birney,E. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Hori,F., Imotani,K.,
Ishi,Y., Itoh,M., Kayashida,K., Hirozane,T., Kojima,Y., Kondo,S., Konno
,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Momura,K.,
Numazaki,R., Ohno,M., Ohasto,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
submission
                                                                                                                                                                                                                                                                                                                                                                                                                              prepare mouse tissues.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computational Analysis of Full-Length Mouse cDNAs Compared with numan Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                      1. .638
                                          /clone="9330209D03"
/sex="male"
tissue_type="diencephalon"/
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                                                                                                                                                                              strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                            61
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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kon. Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiy., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batal
                                                                                                                                                                                                                   BY726858 RIKEN full-length enriched, adult male quadrigemina Mus musculus cDNA clone B230034I03 BY726858
                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 663)
                                                                                                                                          Mus musculus
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                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                         GTCCAGATTGAGCTGTTTGCCCCCCGCCACTCTCCTGCTGCCGGATGCCGTTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                GAACTGCTGTTTGACTGGGGGCACCACGAACTGCACAGTTGGCGACCTTGTGGATCTACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATCAGTTCCATATAAGGAGÁTTCGAAGCCTTACTTCAGÁCCGGGAAGAGCCCCACCTGT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACATACATACGCAACCTTAATGTGGGGATCCTTAGGAAGCTGTCGGATTTTATTGATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
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                                                   Kiyosawa, H
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Hori,F., Imotani,K.,
Ishi,Y., Itoh,M., Kayawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno
,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 visit our web site (http://genome.gsc.riken.go.jp) for
quadrigemina".
                                         /lab_host="DH10B"
/clone_lib="RIKEN
                                                                                                                        tissue_type="corpora quadrigemina"
/dev_stage="adult"
                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="B230034I03"
                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus
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tref="+-
                                         full-length enriched,
                                              adult male
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 CAAGAAGGGTGGAAGAAATTAGCAGTAGCTATCAAAAAAGCCGTCCGGCGACGACAGATAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 AsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSerProThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr
                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 676)

Arakawa T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, P., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasah, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagamai, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Tayamatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                       BB613167 RIKEN full-length enriched, 10 day neona musculus cDNA clone 4732460109 5', mRNA sequence.
               RIKEN Mouse ESTs (Arakawa, T., Unpublished
                                                                                                                                                                                                                                                                                                                         BB613167
                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                Mus musculus (house mouse)
Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugging and Taranachianti.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
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                                                                                                                                                                                                                    /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                contributed to prepare
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/lab_host="DH10B"
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/mol_type="mRNA"
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'clone="4732460109"
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, T., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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High-efficiency full-length cDNA
Meth: Enzymol. 303, 19-44 (1999)
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Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
On Oct 4, 2001 this sequence version replaced gi:12860970. Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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6 (bases 1 to 1161)
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/tissue_type="diencephalon"
/clone_lib="RIKEN_full-length_enriched_mouse_cDNA_library"
/dev_stage="adult"
183. .776
                                                                                                                                                                  /db_xref="FANTOM_DB:9330209D03"
/db_xref="MGI:1911393"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                     location/Qualifiers
                                                                                                                                                                                                                                                           strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                sex="male"
                                                                                                                                          clone="9330209D03"
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                                              Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                               AK028837

2481 bp mRNA linear HTC 05-DEC-2002
Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
library, clone:4732460109 product:interleukin-l receptor-associated
kinase 4 [Mus musculus], full insert sequence.
                                  20499374
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                HTC; CAP trapper.
                                                                                                                                                                                                                         Carninci, P. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
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/db_xref="G1:15919912"
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DDRYNOPHIRREEALLOTGKSPTCELLFDWGTTNCTVGDLVDLLVQIELFAPATLLLP
DAVPQTVKSLPPKEAGNSGTNTRALSGKGQDIRNAYAKTRTQLRATGLLSPDNRSVES
SDTRFHSFSFHELKSITNNFDSDPASAGGNRWGEGGF"

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receptor-associated kinase 4 [Mus musculus]
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Shibata, K.,

Itoh, M.,

Aizawa, K., Nagaoka, S.,

Sasaki, N.,

Carninci, P.,

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                                                                                                                                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                          URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
                                                                                                                                                                                           prepare mouse tissues.
Please visit our web site for further details
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax:81-45-503-9216)
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Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning
                                                                                                                                                                                       AK029028 2810 bp mRNA linear HTC 05-DEC-2002 Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732482P03 product:interleukin-1 receptor-associated kinase 4 [Mus musculus], full insert sequence.
                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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/db_xref="G1:26324784"
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/translation="makeutpestyiraliavgilrklsdfiddogegwkklavaikkpsg
DDRYNQFHIRRFEALLQTGKSPTCELLFDWGTTNCTVGDLVDLLVQIELFAPATILLP
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SDTRFHSFSFHELKSITNNFDEQPASAGGNRMGEGGFGVVKSCEVNNTIVAVKKLARLSC
SDTRFHSFSFHELKSITNNFDEQPASAGGNRMGEGGFGVVLCYKGCVNNTIVAVKKLARLSC
LDGTPPLSWHTRCKVAQGTANGIRFLHENHHIHRDIKSANILLDKDFTAKISDFGLAR
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10 days neonate"
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                                                                                                                                                            Adachi, J., Aliawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P. Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Muzzaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Sakai, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muratatu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 2810)
Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama.
                                                                 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
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CDNA library was prepared and sequenced in Mouse Genome cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Please visit our web site for further details.
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Mus musculus (house mouse)

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Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
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RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
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-DB=M Geneseq_19Jun03 -QFMT=fastap_-SUFFIX=rng_-MINMATCH=0.1 -LOOFCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10001254 @CGN 1 1 0 @runat 16012004 152423 19704 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0-MAIT.-DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT

2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT

3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT

3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT

4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT

5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT

6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT

7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT

8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT

9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT

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11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT

12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT

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score Pred. No. is the number of results predicted by greater than or equal to the score of the chance to hav have printed,

> and is derived by analysis of the total score distribution.

SUMMARIES

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ABZ14172	ABZ13465	AAL45902	AAC46629	ABZ13385	AAC39626	AAC41148	ABZ12535	AAC47551	AAC35365	AAC42305	ABZ13464	ABZ12819	AAC37541	AAL45898	AAA11352	AAC42456	ABZ12994	ABZ13868	AAC49420	ACAS6495	ABL62666	ABN95724	ABK83909	ABZ34976	AAT62551	AAD40074	AAS76802	AAS61608	ABQ92043	AAV63193	AAH09161	AAF22511	AAF22618	ABL90822	ARK43727	ABK44003	AAS27214	AAA09319	AAS76805	AAH13798	AAD10198	AAD40085	AAD10197	AAD40079	10	;
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ALIGNMENTS

AAD40079 standard; DNA; 1383 BP.

AAD40079;

22-OCT-2002 (first entry)

Human IRAK4 gene #1.

RESULT 1
AAD40079
'ID AAD4
XX
AC AAD4
XY
CAC AAD4
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Huma
XX
Hoffl Human; death domain; DD; death effector domain; DED; Chlamydia infection; NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autroimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; Homo sapiens. immunosuppressive; gene therapy; antisense therapy; gene; ds

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                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                 The invention relates to an isolated polypeptide comprising a death CC domain (DD), death effector domain (DD) or NB-ARC domain. The invention CC is useful for identifying a binding agent, preferably a protein or a drug CC that binds a DD, DED or NB-ARC domain, by contacting a DD protein) or NB-ARC Contacting a DD protein). DED or NB-ARC domain for moments and CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED or NB-ARC CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent, or chemical crosslinking, nuclear magnetic resonance (NMR), mass content of two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or CC interpretation (MS) and FPA. The invention is useful for modulating the CC level of a cell process such as cell proliferation, cell adhesion, cell immunoglobulin class switching, in particular apoptosis within a cell. CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the CC invention is useful for modulating the activity of oncogenic proteins. The protein and antibody specific for it are useful for creating bacterial infections by modulating the activity of bacterial CC proteins. The protein and antibody specific for it are useful for it suseful for treating immune-based pathologies, pathologies associated CC with cell division, inflammatory diseases such as sepsis, fibrosis, cc therapy and gene therapy. The present security is useful for atherapy and gene therapy. The present security is useful for artivity of pathologies.
                                                                     US-10-001-254-16 (1-460)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases
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                                            ArgGlyGluIleThrProLysSerAspIleTyrSerPheGlyValValLeuLeuGluIle
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The present sequence is a cDNA encoding human interleukin (II)-1 recept associated kinase (IRAK)-4. IRAK associate with activated II-1, II-18 and other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)-kappaB activation. The IRAK-4 inhibitors are useful for treating inflammatory diseases such as pulmonary diseases and diseases of the airway (e.g., adult respiratory
                                                                                                                                                            Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating asthma, allergic rhinitis, multiple sclerosis and skin cancer -
                                                                                                                                 Claim
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CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough CC or allergic rhinitis), transplant rejection, autoimmune diseases (e.g., CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis CC or diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma), CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases CC of the central nervous system (e.g., neurodegenerative disease), CD14 CC mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoprosis, CC psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and CC culcarative colitis), Behcet's syndrome, antylosing spondylitis, gout, Sarcoidosis and ophthalmic diseases and conditions. The inhibitors of CC rank-4 activity or expression are used to inhibit signal transduction CC resulting from the activation of an interleukin-1 receptor (IL-IR)/Toll receptor in a cell. They also inhibit the activation of a transcription CC ractor that activates NFkappaB in the cell. IRAK-4 is used to create a conditions and conditions and for the study of inflammatory CC disorders and conditions and for the development of potential treatments for IRAK-4 related in flammatory diseases and conditions. IRAK-4 sequences
  Sequence 1383
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Best Local Similarity: Query Match: 1.69e-233 2382.00 99.78% 99.78% 99.83% Gaps: Mismatches: Indels:

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                                                                                                 NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy; gene; ds.
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CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention contribution (DED) or NB-ARC domain. The invention contribution is useful for identifying a binding agent, preferably a protein or a drug contribution of the binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC comain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED or NB-ARC contribution of the domain and the candidate binding agent, by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NMR), mass contention is useful for modulating the contibution of a cell process such as cell proliferation, cell adhesion, cell immunoglobulin class switching, in particular apoptosis within a cell. Cc immunoglobulin class switching, in particular apoptosis within a cell. Cc muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the crownian. The protein is useful for modulating the activity of nocogenic proteins. The contribution is useful for modulating the activity of nocogenic proteins. The protein and antibody specific for it are useful for cc treating bacterial infections by modulating the activity of bacterial contribution. Inflammatory diseases such as sepsis, fibrosis, autoimmunity, allograft rejection and other diseases. The protein contribution, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense cc ct therapy and gene therapy. The present sequence is human IRAK4 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases
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29-JUN-2001; 2001US-301889P.
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ATAACTGGACTTCCAGCTGTGGATGAACACCGTGAACCTCAGTTATTGCTAGATATTAAA
                   IleThrGlyLeuProAlaValAspGluHisArgGluProGlnLeuLeuLeuAspIleLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic; II, antibacterial, antiinflammatory; ophthalmological; vasotropic; OPD; chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermaticis; inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis; Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/foll receptor; sarcoidosis; transgenic animal; ss.
                                                                                                                                                                      Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating asthma, allergic rhinitis, multiple sclerosis and skin cancer -
                                                                                                                                                                                                                            P-PSDB; AAE05399.
                                                                                                                                                                                                                                                                                                                     13-JAN-2000; 2000US-0176395.
                                                                                                                                                                                                                                                                                                                                               12-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 cDNA.
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The present sequence is a cDNA encoding mouse interleukin (IL)-1 recept associated kinase (IRAK)-4. IRAK associate with activated IL-1, IL-18 and other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)-kappaB activation. The IRAK-4 inhibitors are useful for treating inflammatory diseases such as pulmonary diseases and diseases of the airway (e.g., adult respiratory disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD), pulmonary fibrosis, interstitial lung disease, asthma, chronic cough or allergic rhinitis), transplant rejection, autoimmune diseases (e.g., (IL)-1 receptor

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1542 BP; 421 A; 392 C;
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TyrLysGlyTyrValAsnAsnThrThrValAlaValLysLysLeuAlaAlaMetValAsp
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                                                 GACGAGCAACCCGCGTCTGCCGGTGGCAACCGGATGGGAGAGGGGGGATTTGGAGTGGTG
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29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                             Human cDNA sequence SEQ ID NO:10742.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of a polynucleotide comprises one of oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide sequences defined in the specification, where the off of the comprises at least 15 nucleotides; or (b) a combination complementary strand of comprising a sequence commission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are useful for the seful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH13632 to AAH13632, all of which are used in the exemplification of the numer times.
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   LeuProAspAla-ValProLysThrAlaAsnThrLeuProSerLysGluAlaIleThrVa
                                                                           ValGlyAspLeuValAspLeuLeuIleGlnAsnGluPhePheAlaProAlaSerLeuLeu
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T, Wakamatsı
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                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. (CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC anino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed contribution, but was obtained in electronic format directly from WIPO CC at fer, wino, intrub/published not segmences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess highly responsible.
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                          No.:
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                LysProSerGlyAspAspArgTyrAsnGlnPheHisIleArgArgPheGluAlaLeuLeu
                                                                              LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLysLeuAlaValAlaIleLys
                                                             AAGCTGTCAGATTTTATTGATCCTCAAGAAGGATGGAAGAAGTTAGCTGTAGCTATTAAA
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                                                                                                                             ATGAACAAACCCATAACACCATCAACATATGTGCGCTGCCTCAATGTTGGACTAATTAGG
AAACCATCTGGTGATGATAGATACAATCAGTTTCACATAAGGAGATTTGAAGCATTACTT
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                                        GluGluIleGluAspGluGluLysThrIleGluAspTyrIleAspLysLysMetAsnAsp
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               TCCAAATGTGAAGAAAAGCTGATGTTTTAAGCTCCTTTTTGGATGAAAAAACTCATGAG
                                                                                                                                             CGTGGAGAAATAACACCCAAATCTGATATTTACAGCTTT-----
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                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                 AAA09310-20 are novel genes isolated by SEREX screening from a renal cancer cell line 1973/10.4. The genes encode cancer associated antigen precursors. These gene products are useful in methods for preventing, diagnosing and/or treating disorders, especially cancer, associated with abnormal expression of human cancer associated antigens. The method comprises contacting a sample from a subject with an agent that specifically binds to the nucleic acid molecule or expression product specifically binds to the nucleic acid molecule or expression product
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 57; Page 85; 121pp; English.
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abnormal expression
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                                                                                                                                                                                                                                                                             fragment) complexed with a human leukocyte antigen (HLA) molecule determining the interaction between the agent and the nucleic acidecule or the expression product as a determination of the disorder
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DB; AAY92347.
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                                                                          ATGAACAAACCCATAACACCATCAACATATGTGCGCTGCCTCAATGTTGGACTAATTAGG
                                                                                       MetAsnLysProIleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg
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E, Chen Y,
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                                                                                              Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS; ss;
                                                                                                                                                                                                                                                   cDNA encoding novel signal transduction pathway protein,
                                                                                                                                                                                                                                                                                                               AAS27214;
                                                                                                                                                                                                                                                                                                                                              AAS27214 standard; cDNA; 1493
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NS-0229 NS-0249 NS-0250 NS-0250 NS-0251	2000US-0236369. 2000US-0236370. 2000US-0236370. 2000US-0237039. 2000US-0237039. 2000US-0237039. 2000US-0241960. 2000US-0241785. 2000US-0241786. 2000US-0241879. 2000US-0241879. 2000US-0241879. 2000US-0241870. 2000US-024674. 2000US-024677. 2000US-024677. 2000US-024677. 2000US-024677. 2000US-024678. 2000US-024971. 2000US-024971. 2000US-024971. 2000US-024971.

31-JAN-2000 24-FEB-2000 20-MAR-2000 11-MAR-2000 11-MAR-2000 11-JUN-2000 21-JUN-2000 21-JUN-2000 21-JUN-2000 21-JUL-2000 11-JUL-2000 11-JU

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC The invention relates to novel isolated polypeptides (I), and CC polynucleotides (II). (II) (II) and the antibody to (I) are useful for CC diagnosing, preventing and treating diseases including immune system CC disorders (e.g. congenital and acquired immundeficiencies, autoimmune CC transplant rejections and graft versus host disease, infectious diseases CC (e.g. hepatitis (), bleeding disorders, haemoglobin abnormalities and CC other blood-related disorders (sickle cell anaemia), myeloproliferative CC disorders, primary haematopoietic disorders, hyperproliferative CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative CC disorders (e.g. Gaucher's disease), rarkinson's disease), chromosomal CC disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. dadison's disease), reproductive system disorders, gastrointestinal CC disorder (inflammatory disorders), liver disorders, gastrointestinal CC disorder (inflammatory disorders), liver disorders, activators of CC T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency cyndrome (AIDS). AAS26976-AAS27850 represent novel signal transduction.
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                               GluAspTyrIleAspLysLysMetAsnAspAlaAspSerThrSerValGluAlaMetTyr
                                                                                                  ArgGluProGlnLeuLeuLeuAspIleLysGluGluIleGluAspGluGluLysThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyLeuAlaArgAlaSerGluLysPheAlaGlnThrValMetThrSerArgIleValGly
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GAAGATTATATTGATAAAAAGATGAATGATGCTGATTCCACTTCAGTTGAAGCTATGTAC
                                                                                                                                                                                                                TACAGCTTTGGTGTGTTTTACTAGAAATAATAACTGGACTTCCAGCTGTGGATGAACAC
                                                                                                                                                                                                                                               TyrSerPheGlyValValLeuLeuGluIleIleThrGlyLeuProAlaValAspGluHis 390
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ID ABK4400
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XX ABK440
XX ABK440
XX DNA en
XX DNA en
XX Centra
KW Centra
KW Acquir
KW acquir
KW acquir
KW acquir
KW acquir
KW endocr
KW endocr
KW food a
XX 17-JAN
XX 70-JUN
PR 10-JUN
PR 11-JUL
PR 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUL-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
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2000US-0226681.
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2000US-0217496.

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2000US-0225270.
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2000US-0225213.
2000US-0225214.
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Alignment
Pred. No.:
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                                                                                                                                                                                          The invention describes an isolated nucleic acid molecule (I) encoding a convel central nervous system protein. (I) and polypeptides (III) encoded (I) are used to treat a medical conditions and in diagnosis of a gathological condition. Disorders which are diagnosed or treated include constituen. Disorders which are diagnosed or treated include cardiname diseases e.g. rheumatoid arthritis, hyperproliferative conditions and in claude autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative conscious cardiac arrest, cerebrovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. and function caused by bacteria, viruses conscious infection, gastrointestinal disorders e.g. dysphagia, corneal infection, and crimatorine disorders e.g. diabetes can pituitary dwarfism, cancers and disorders at the cellular level e.g. corneal infection. The polypeptides can also be used disorders e.g. myocardial corneave transplantation, for supporting due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The colypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used food additives or preservatives -
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                                                                                                                                                                                                                                                                             Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AlbS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging;
         31-JAN-2000;
04-FEB-2000;
                                                                        17-JAN-2001; 2001WO-US01332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding novel central nervous system protein #307.
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02-MAR-2000;
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18-APR-2000;
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2000US-022963.
2000US-0224518.
2000US-0224518.
2000US-02252513.
2000US-0225214.
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2000US-0225266.
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21-NOV-2000)
21-NO
               New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and food additives or preservatives -
                                                                                P-PSDB;
                                                                                2001-581633/65.
DB; AAU87397.
                                                                                                                                                                 HUMAN
                                                                                                                               Barash SC,
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                                                                                          | GluAspTyrIleAspLysLysMetAsnAspAlaAspSerThrSerValGluAlaMetTyr
                                                                                                                                                                 ArgGluProGlnLeuLeuLeuAspIleLysGluGluIleGluAspGluGluLysThrIle
                                                                                                                                                                                                                                  TyrSerPheGlyValValLeuLeuGluIleIleThrGlyLeuProAlaValAspGluHis
                                                                                                                                                                                                                                                                                                            ThrThrAlaTyrMetAlaProGluAlaLeuArgGlyGluIleThrProLysSerAspIle
                                                                                                                                                                                                                                                                                                                                                                           GlyLeuAlaArgAlaSerGluLysPheAlaGlnThrValMetThrSerArgIleValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                AspIleLysSerAlaAsnIleLeuLeuAspGluAlaPheThrAlaLysIleSerAspPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IleAlaGlnGlyAlaAlaAsnGlyIleAsnPheLeuHisGluAsnHisHisIleHisArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID
                       SerValAlaSerGlnCysLeuHisGluLysLysAsnLysArgProAspIleLysLysVal
                                                                          GAAGATTATATTGATAAAAAGATGAATGATGCTGATTCCACTTCAGTTGAAGCTATGTAC
                                                                                                                                              CGTGAACCTCAGTTATTGCTAGATATTAAAGAAGAAATTGAAGATGAAGAAAAGACAATT
                                                                                                                                                                                                                 TACAGCTTTGGTGTGTTTTACTAGAAATAATAACTGGACTTCCAGCTGTGGATGAACAC
                                                                                                                                                                                                                                                                                    ACAACAGCTTATATGGCACCAGAAGCTTTGCGTGGAGAAATAACACCCAAATCTGATATT
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Conservative:
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       542
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GlnGlnLeuLeuGlnGluMetThrAlaSer

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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                            Alignment Scores
                                                                             Pred. No.:
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                                                                                                                                                                                                        (ABBB9040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (anti-agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial isohaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                       Sequence 1181
                                                                                                                                             Note: The sequence data for this patent did not form part printed specification, but was obtained in electronic form from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                        epilepsy; and (f) intecti
and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; SEQ ID NO 1384; 2081pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel 1405 isolated polypeptides, useful for diagnosis, treatment an prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cycostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
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DB; ABB90413.
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                                                                                                                                                                                                                                                                                                                                                                                                                 relates to novel genes (ABL89449-ABL90853) and
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Matches:
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RESULT 12
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Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition
                                      WPI; 2001-025274/03
                                                                                                             28-MAY-1999;
10-SEP-1999;
                                                                                                                                                                         07-DEC-2000
                                                                                                                                                                                                                                                 Human; breast cancer; gastric cancer; prostate cancer; diagnosis; cancer associated antigen; cytostatic; cancer vaccine; ss.
                                                                                                                                                                                                                                                                                                               26-MAR-2001
                                                                                                                                                                                                                                                                                                                                    AAF22618;
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                                                                                                                                                                                                                          Homo sapiens.
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99US-0153454.
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RESULT 13
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ID AAF22
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AC AAF22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63221 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
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 Human breast cancer associated antigen nucleotide sequence SEQ ID NO:90.
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                         26-MAR-2001
                                                 AAF22511;
                                                                        AAF22511 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.:
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                                                                                                                     SMETASDASPALAASPSETTHYSEYVALGIUALAMETTYY-SEYVALALASEYGINCYS 436
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                                                                                                                                                                                AspIle-LysGluGluIleGluAspGluGluLysThrIleGluAspTyrIleAspLysLy
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97.24%
37.01%
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Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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Human;
cancer
Nucleic acids encoding breast, gastric and prostate cancer associantigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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10-SEP-1999;
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                                                                                                     WPI; 2001-025274/03
                                                                                                                                                                                                      (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     breast cancer; gastric cancer; prostate cancer; associated antigen; cytostatic; cancer vaccine;
                                                                                                                                                                                                                                                        99US-0136526.
99US-0153454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis;
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Claim 50; Page 303; 799pp; English

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represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively.

AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence production. CAAPs have cytostatic activity and can be used in the prospectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic actis or anti-CAAP antibodies are useful for diagnosing and treating a AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 condition characterised by expression of an abnormal amount of a protein,

Sequence 586 BP; 183 A; 103 Ç 120 G; 173 7; 7 other;

8.07e-81 883.00 97.24% 97.24% 37.01%

Matches: Conservative: Mismatches: Indels:

586 176 0

Gaps:

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358 GluAlaLeuArgGlyGluIleThrProLysSerAspIleTyrSerPheGlyValValLeu 377	288 AAGTTTGCCCAGACAGTCATGACTAGCAGAATTGTGGGAACAACAGCTTATATGGCACCA 347	338 LyspheAlaGlnThrValMetThrSerArgIleValGlyThrThrAlaTyrMetAlaPro 357	228 TTACTGGATGAAGCTTTTACTGCTAAAATATCTGACTTTGGCCTTGCACGGCTTCTGAG 287	318 LeuLeuAspGluAlaPheThrAlaLysIleSerAspPheGlyLeuAlaArgAlaSerGlu 337	168 GGCATCAATTTTCTACATGAAAATCATCATATTCATAGAGAGATATTAAAAGTGCAAATATC 227	298 GlyIleAsnPheLeuHisGluAsnHisHisIleHisArgAspIleLysSerAlaAsnIle 317	108 GATGGTACTCCACCACTTTCTTGGCACATGAGATGCAAGATTGCTCAGGGTGCAGCTAAT 167	278 AspGlyThrProProLeuSerTrpHisMetArgCysLysIleAlaGlnGlyAlaAlaAsn 297	48 CTCTGCTTAGTATATGTTTACATGCCTAATGGTTCATTGCTAGACAGAC	258 LeuCysLeuValTyrValTyrMetProAsnGlySerLeuLeuAspArgLeuSerCysLeu 277	US-10-001-254-16 (1-460) x AAF22511 (1-586)

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RESULT 14
AAH09161/c
ID AAH091
XX AAH091
XX Human
XX Human;
XX Human;
XX Homo s
XX Hom
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The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the CC coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end sequence complementary to a coligonucleotide which comprises a 3'-end sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC cligonucleotide comprises a selected from those defined in CC the 5'-end sequence). The primers sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by CC detection and/or diagnosis of the abnormality of the proteins encoded by CC daylisas asily without any specialised methods. AAH03166 to AAH13628 and CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing full-length cDNAs defined in and/or diagnosis of the abnor full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3;
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Homo

sapiens.

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US-10-001-254-16 (1-460) x AAV63193 (1-483)
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Best Local Similarity:
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25-MAR-1998;
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P-PSDB; AAW80409.
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pIleTyrSerPheGlyValValLeuLeuGluIleIleThrGlyLeuProAlaValAspGl 389
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Search completed: January 18, Job time: 567.702 secs 01:32:15

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Title:
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-Q=/cgn2 1/USPTO_spool/US10001254/runat 16012004 152423 19714/app_query.fasta_1.1109
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZES=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10001254 @CGN 1 1 5671 @runat 16012004 152423 19714 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPPEXT=0.5 -DELOP=6 -DELEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

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Query Match Length DB

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ALIGNMENTS

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241 GTTGGTGATCTTGTGGATCTTTTGATCCAAAATGAATTTTTTTT	61 GlnThrGlyLysSerProThrSerGluLeuLeuPheAspTrpGlyThrThrAsnCysThr 80	AspaspargTyrasnGlnPheHislleargargPheGlua	MetAsnLysProIleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg	100.00% Indels: 6 Gaps: 0) x AX431306 (1-1383)	Arigiment Scores: 4.99e-198 Length: 1383 Score: 2386.00 Matches: 460 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0	463 a 243 c 283 g 394 t	LOGTEPLEMENT CHARACTERMENT FEBRUARY STATEMENT OF A PREMISE RESIDENCE OF A PREMISE REPORT OF A PREMISE REPORT OF A PREMISE REPORT OF A PROPERTY OF A PROPERTY OF A SEKFAQTVMTSRIVGITAYMAPEALRGEITPKSDIYSFGVVLLEIITGLPAVDEHRE POLLLDIKESIEDEEKTIEDYIDKKMNDADSTSVEAMYSVASQCLHEKKNKRPDIKKV OOLLOEMTAS F	DDRYNGHIRREALLLOTGKSEPTSELLEDWGTTNCTVCDLUVDLLQUEFRARASLLLE DAVPKTANTLESKEAITVQQKQMPFCDKDRTLMTPVQNLEQSYMPPDSSSPENKSLEV SDTREELSFSYELKNVINNEDERPISVGANKGEGGFGVVYKGYVNNTTVAVKKLAAM SDTREELSFSYELKNVINNEDERPISVGANKGEGGFGVVYKGYVNNTTVAVKKLAAM	/ note - unitalized for the following for the fo	/originates: nonce original forms / mol type="genomic DNA" / db_xref="taxon:9606" 1.	BURNHAM INST (US) Location/Qualifiers 1. 1383	Pawlowski,K., Fiorentino,L., Godzik,A., Lee,S.H., Reed,J.C., Roth,W. and Stenner-Liewen,F. Novel death domain proteins Parent: WO 0.240680-A 15 23-MAY-2002.	Homo sapiens Eukaryota; Me Mammalia; Eut	AX431306 AX431306.1 GI:21656175	
RESULT 2 BC013316 LOCUS LOCUS DEFINITION ACCESSION VERSION		D Q	оь Qу	Q B Qy	Qy da	. QQ	D Q	Db Qy	dd Vŷ	Qy db	B Q	D Qy	B &	gg Qy	Db
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JOURNAL
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131
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7705
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (31-AUG-2001) National Institutes of Health, Mammalian Submitted (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey,
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: CLONTECH Laboratories, IncDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Institute for Systems Biology
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NIH-MGC Project URL: http://mgc.nci.nih.gov
COntact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laborator
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                                                             MetAsnLysProIleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg
               LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLys
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mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1_to 1629)
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DDRYNQFHIRREALLQTGKSPTSELLEPWGTTWCTVGDLVDLLIQNEEFAPASLLLP
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PQLLLDIKEEIEDEEKTIEDYIDKKMNDADSTSVEAMYSVASQCLHEKKNKRPDIKKV
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/db_xref="GI:15426432"
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/tissue type="Brain, primitive ne
/clone Tib="NIH MGC_56"
/lab host="UH108"
/note="Vector: pDNR-LIB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Deptment of Virology; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
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Sugano, S., Suzuki, Y., Ota, T.,
Shibahara, T., Tanaka, T. and Na
Direct Submission
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Nakamura,Y., Isogai,T. and Sugano,S.
NBDO human cDNA sequencing project
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QQLLQEMTAS"
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/codon_start=1
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/db_xref="taxon:9606"
/clone="KAT10395"
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ASEKFAQIYMTSRIVGTTAYWAPEALRGEITPKSDIYSFGVVLLEIITGLPAVDEHRE PQLLLDEMTAS" 244 c 283 g 393 t 1.11e-197 Length: 1383 2.382.00 Matches: 459 99.78% Mismatches: 0 99.78% Mismatches: 1 99.83% Indels: 0	m="Ho e="ge e="tax uman uman tart= id="" id="" Tion= IRRFE IRRFE TLPSK KQQFD KQQFD	0 1383 e 2 from Patent WO015 0 0.1 GI:15386462 piens (human) piens (ta; Metazoa; Chordata a; Eutheria; Primates H. and Li,S. compositions and met WO 0151641-A 2 19-JU Inc. (US) Location/Qualifiers 1. 1383	 ACTGCTA ACTGCTA MetThrs 1 1 1
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Suzuki, N., Duncan, G.S., Millar, D.G., Wada, T., Mirtsos, C., Takada, H., Wakeham, A., Itie, A., Li, S., Penning Wesche, H., Ohashi, P.S., Mak, T.W. and Yeh, W.C.
Severe impairment of interleukin-1 and Toll-like receptor signalling in mice lacking IRAK-4
Nature 416 (6882), 750-756 (2002)
                                                                                                                                                                                                  Li,S., Strelow,A., Fontana,E.J.
Direct Submission
Submitted (08-NOV-2001) Biology
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Homo sapiens interleukin-1 receptor
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IRAK-4: a novel member
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translation="MNKPITPSTYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDRYNQFHIRRFEALLQTGKSPTSELLFDWGTTNCTAGDLVDLLIQNEFFAPASLLLFDWGTTNCTAGDLVDLLIQNEFFAPASLLLPDWGTTNCTAGDLVDLLIQNEFFAPASLLLPDWGTTNTPVQNLEQSYMPPDSSSPENKSLEV
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QQLLQEMTAS"

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US-10-001-254-16 (1-460) x AF445802 (1-1383) Percent Similarity:
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Query Match:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps: 001 100 260 240 660 600 540 180 480 160 420 140 360 120 80 60 120 40 720 220 200 300 240 180 60 20

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Scanlan,M.J., Gordan,J.D., Williams
Jongeneel,V., Gure,A.O., Jager,D.,
and Old,L.J.
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Scanlan, M.J., Gordan, J.D., Williamson, B., Stockert, E., Jongeneel, V., Gure, A.O., Jager, D., Jager, E., Knuth, A., and Old, L.J.
                                                                                                                                                                                                                                                                                                                                                      Homo
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AF155118
                                                                                                                                        Submitted (28-MAY-1999) Ludwig Institute, Sloan-Kettering Institute, 1275 York Ave, New York, NY 10021, USA
                                                                                                                                                                                                                                                         Antigens recognized by autologous antibody renal-cell carcinoma
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/codon_start=1
/product="putative protein
/protein_id="AAD42884.1"
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                                               /cell_type="renal cell carcinoma"
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                                                                                                                               Location/Qualifiers
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ASEKFAQTVMTSRIVGTTAYMAFEALRGEITPKSDIYSFGVVLLEIITGLPAVDEHRE
PQLLLDIKEELEDEEKTIEDYIDKKMNDADSTSVEAMYSGASQCHHEKKNKSPDIKKV
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Eutheria;
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Rodentia;
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883 CAGCACGAGAACCTGGTGGAGCTGCTCGGCTTCTCCAGCGACAGCGACAACCTGTGCTTA 9	븅
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221 118"INT'INTGIUGIULEULYSGINGINPHEASPGINGIUILELYSVAIMECALALYSCYS 240 :::	B &
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703 GACGAGCAACCCGCGTCTGCCGGTGGCAACCCGGATGGGAGAGGGGGGATTTGGAGTGGTG 76	Db .
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141 LeuGluGlnSerTyrMetProProAspSerSerSerProGluAsnLysSerLeuGluVal 160	δõ
523 GCACAAACACACGGGCCTTGTCAGGAAAAGGACAGGACA	뫄
121 GlnGlnI	Ş
463 CIGCCGGATGCCGTTCCCCAA	맑
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21 LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLys 40	; 15
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                                                                                                                                              Submitted (08-NOV-2001) Biology South San Francisco, CA 94080,
                                                                                                                                                                     Li,S., Strelow,A., Fontana,E.J. and Direct Submission
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Mammalia; Eutheria; Rodentia;
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strain="BALB/c"
                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                 (house mouse)
                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                  99
                                                                                                                                                USA,
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                                                                                                                                                          Tularik Inc.,
                                                                                                                                                                                   Wesche,
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                                                                                                                                                                                                                                  (2002)
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Query Match:
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                                                                                                                                                                                                                                                                                                          463
                                                                                                            703
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QQLLQEMSA" a 392 c /product="interleukin-1 receptor associated kinase 4"
/protein_id="AAM15773.1"
/db xref="GI:20219012"
/translation="MAKPLIPSTYIRNINVGILRKLSDFIDDQEGWKKLAVAIKKPSG
DRYNOPHIRRFEALLQTGKSPTCELLFDWGTTNCTVGDLVDLLVQIELFAPATLLLF
DAVPQTVKSLPPREATVAQTHGPCQEKDRYSVMPNFKLEHSCEPDSSSPDNRSVES
SDTRFHSFSFHELKSITNNFDEDPALSGGEROFVVKGCVNNTIVALKLGAM
VEISTELKQGPOPGEIKVAFTCQHENLVELLGFSSDSDNLCLVAYAYNDNGSLLDRLSC
LDGTPPLSWHTRCKVAQGTANGIRFLHENHHIHRDIKSANILLDKDFTAKISDFGLAR
ASARLAQTVNTSRIVCTTAYMAPEALRGEIFPKSDIYSFGVVLLELITGLAANDENRE PQLLLDIKEEIEDEEKTIEDYTDEKMSDADPASVEAMYSAASQCLHEKKNRRPDIAKV

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US-10-001-254-16 (1-460) x AF445803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MetAsnLysProlleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg
                                                           LeuGluGlnSerTyrMetProProAspSerSerSerProGluAsnLysSerLeuGluVal
                                                                                                                                                                                                                                                                                                                                                            GlnGlnLysGlnMetProPheCysAspLysAspArgThrLeuMetThrProValGlnAsn
                                                                                                                                                                                                                                                                                                                                                                                                                       LeuProAspAlaValProLysThrAlaAsnThrLeuProSerLysGluAlaIleThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValGlyAspLeuValAspLeuLeuIleGlnAsnGluPhePheAlaProAlaSerLeuLeu
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                                                                                                                               GACGAGCAACCCGCGTCTGCCGGTGGCAACCGGATGGGAGAGGGGGGATTTGGAGTGGTG
                                                                                                                                                 SerAspThrArgPheHisSerPheSerPheTyrCluLeuLysAsnValThrAsnAsnPhe
                                                                                                                                                                                                                                                                                                                                     CTGCCGGATGCCGTTCCCCAAACCGTCAAAAGCCTGCCTCCTAGAGAAGCGGCAACAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTGGCGACCTTGTGGATCTACTGGTCCAGATTGAGCTGTTTGCCCCCCGCCACTCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGACCGGGAAGAGCCCCACCTGTGAACTGCTGTTTGACTGGGGCACCACGAACTGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGCCGTCCGGCGACGACAGATACAATCAGTTCCATATAAGGAGATTCGAAGCCTTACTT
                 IleThrThrGluGluLeuLysGlnGlnPheAspGlnGluIleLysValMetAlaLysCys
                                                                                                                                                                                                                                                                    CTAGAACACAGCTGCGAGCCACCGGACTCCTCAAGCCCAGACAACAGAAGTGTAGAGTCC
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2017.00
90.85%
83.88%
84.53%
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Matches:
Conservative:
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882
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AUTHORS
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BC051676
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S. F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R. F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T. E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E. J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevcherko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   variant 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluGluIleGluAspGluGluLysThrIleGluAspTyrIleAspLysBLysMetAsnAsp 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATAACCGGGCTGGCGGCTGTGAAAAACCGTGAACCTCAACTACTGCTGGATATTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGACGGTCATGACCAGCCGAATCGTGGGCACAACGGCTTACATGGCACCCGAAGCTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTCTGCATGAAAATCATCACATTCATAGAGATATTAAAAGTGCAAATATCTTACTAGAC
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                                                                                                                                                                                                                                                                                                                                                                           nmalia; Eutheria;
(bases 1 to 2431)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:30354527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2431 bp mRNA linear ROD 10-JUN-2003
interleukin-1 receptor-associated kinase 4, transcript
RNA (cDNA clone MGC:60994 IMAGE:30017484), complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse)
                                                                                                                                                                                                                                                                                                                                                                                                    Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1482
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MEDLINE
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            Alignment Scores: Pred. No.:
                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
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JOURNAL
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Clone distribution: MGC clone distribution information can be founthrough the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAK Plate: 111 Row: i Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23943897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.
Contact: MGC help desk
Email: cgpbs-r@mail.nih.gov
Tissue Procurement: Minoru Ko
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Submitted (30-APR-2003) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Yulan Piao and Minoru Ko cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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a 580 c
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ASARLAQTVMTSRIVGTTAYWAPEALAGEITPKSDIYSFGVVLLELITGLAAVDENRE
PQLLLDIKEBIEDEEKTIEDYTDEKWSDADPASVEAMYSAASQCLHEKKNRRPDIAKV
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(Lona)"
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                                                                                                                                                                                                                                                                                                                                        /protein_id="AAH51676.1"
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D.M., Nanavati,
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 GluAlaPheThrAlaLysIleSerAspPheGlyLeuAlaArgAlaSerGluLysPheAla 340
                                                                                                                                                                                   ValTyrValTyrMetProAsnGlySerLeuLeuAspArgLeuSerCysLeuAspGlyThr 280
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                                                     PheLeuHisGluAsnHisHisIleHisArgAspIleLysSerAlaAsnIleLeuLeuAsp 320
                                                                                                                                                                                                                                                    GlnHisGluAsnLeuValGluLeuLeuGlyPheSerSerAspGlyAspAspLeuCysLeu 260
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                                                                                                 CCACCGCTTTCCTGGCACACAAGGTGCAAGGTTGCTCAGGGGACAGCAAATGGCATCAGG
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1 (bases 1 to 2213)

Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J. Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 10633 09-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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JP 2002191363-A/10633.
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TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
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KEIICHI NAGAI,TETSUJI OTSUKI
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Location/Qualifiers
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) MEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, Industry of Tabu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 2213)
Isogai, T. and Otsuki, T.
Direct Submission
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Nishikawa,T.,
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Mammalia; Eutheria;
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/note="cloning vector: pME18SFL3"
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/tissue_type="whole embryo, mainly head"
/clone_lib="HEMBA1"
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/db_xref="taxon:9606"
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Db 410 CÁGCAÁANACÁGATGCCTTTCTGTGACÁAGÁCÁGGACÁTTGATGACACÁCTGTGCÁGAT 469 Qy 141 LeuGluGlnSerTyrMetProProAspSerSerSerProGluAsnLysSerLeuGluVal 160	340 aGlnThrValMetThrSerArgIleValGlyThrThrAlaTyrMetAlaProGluAlaLe 360
Db 350 CTCCCAGATGCTGTTCCCCAAAACTGCTAATACACTTCCTAAAAGAAGCTATAACAGTT Qy 121 GlnGlnLysGlnMetProPheCysAspLysAspArgThrLeuMetThrProValGlnAsn	320 pglualapheThralaLysIleSerAspPheGlyLeuAlaArgAlaSerGluLysPheAl 340
Db 290 GTTGGTGATCTTGTGGATCTTTTTGATCCAAAATGAATTTTTGCTCCTGCGAGTCTTTTG 349 Qy 101 LeuProAspAlaValaroLysThrAlaAsnThrLeuProSerLysGluAlaIleThrVal 120	300 nPheLeuHisGluAsnHisHisIleHisArgAspIleLysSerAlaAsnIleLeuLeuAs 320
Qy 61 GINTERGY LYSSER PROTECTS SECTION ENGAGED IN DGIVING INCASE NO STATE SO CHARLES AND ANALYSES OF THE SO CHARLES AND ANALYSES OF THE SO CHARLES AND ANALYSES OF THE SOCIETY OF THE SOCI	1384 AGIATATGITTACATGCCTAACGGTTCATTGCTAGACAGACTCTCTTGCTTG
41 LysProSerGlyAspAspArgTyrAsnGlnPheHisIleArgArgPheGluAlaLeuLeu	4 TCAACATGAAAACTTAGTAGAACTACTTGGTTTCTCAAGTGATGGAGATGACCTCTGCTT 0 uValTyrValTyrMetProAsnGlySerLeuLeuAspArgLeuSerCysLeuAspGlyTh
21 LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLys 	
US-10-001-254-16 (1-460) x AR223870 (1-833) Oy MetAsnLysProlleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg 20	200 lTyrLysGlyTyrValAsnàsnThrThrValAlaValLysLysLeuAlaAlaMetValAs 220
Alignment Scores: 1.56e-92 Length: 833 Pred. No.: 1169.00 Matches: 246 Score: 1169.00 Matches: 246 Percent Similarity: 93.21% Conservative: 1 Best Local Similarity: 92.83% Mismatches: 8 Query Match: 48.99% Indels: 10 DB: Gaps: 3	160 lserAspThrArgPheHisSerPheSerPheTyrGluLeuLysAsnValThrAsnAsnAh 180
BASE COUNT 273 a 155 c 179 g 226 t ORIGIN	140 nLeuGluGlnSerTyrMetProProAspSerSerSerProGluAsnLysSerLeuGluVa 160
Knuth,A. Renal cancer associated antigens and uses therefor Renal cancer associated antigens and uses therefor Patent: US 6440663-A 10 27-AUG-2002;	IGInGlnLysGlnMetProPheCysAspLysAspArgThrLeuMetThrProValGlnAs 140
unknown. Unknown. Unklassified. 1 (basss 1.to 833) 1 (basss 1.to 833) Scanlan.M.J. Stockert.E. Chen.YT. Old.L.J	912 912 101 LeuProAspAla-ValProLysThrAlaAsnThrLeuProSerLysGluAlaIleThrVa 120 101 LeuProAspAla-ValProCysThrAlaAsnThrLeuProSerLysGluAlaIleThrVa 120 913TGCTGTTCCAAAAGTACGTATACAGTACTACTAAAGAAAG
ITION Sequence 10 from patent US 6440663. SION AR223870 ON AR223870.1 GI:23332452 RDS	21 ValGlyAspLeuValAspLeuLeuIleGlnAsnGluPhePheAlaProAlaSerLeuLeu
	611
Qy 400 sGluGlu 402 Db 1804 AGAAGAA 1810	LysProSerGlyAspAspArgTyrAsnGlnPheHisIleArgArgPheGluAlaLeuLeu 6
Qy 380 elleThrGlyLeuProAlaValAspGluHisArgGluProGlnLeuLeuAspIleLy 400	21 LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLys 40
	1 MetAsnLysProIleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg 20

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                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
CDNA Library Preparation: Dr. Sumio Sugano and Dr. Ko-ichi Ka
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IPAK Plate: 101 Row: m Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                          http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Hel
Madan, Stephanie Rodrigues, Amy Sar
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Submitted (31-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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  /tissue_type="Whole body, adult, (one male including unfertilized eggs)"
/clone_lib="Sugano_Kawakami_zebrafish_DRA"
/lab_host="DH10B"
                                                                                                                                                                                   Location/Qualifiers
                                                                                    clone="MGC:55553
                                                                                                   mol_type="mRNA"
db_xref="taxon:7955"
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GlyTyrValAsnAsnThrThrValAlaValLysLysLeuAlaAlaMetValAspIleThr
                                                           AGGCCACTTTCGGATGGGGCTGCCGGCTGGGCTCTGGAGGGTTCGGAGTGGTGTTCAGA
                                                                                      ArgProIleSerValGlyGlyAsnLysMetGlyGluGlyGlyPheGlyValValTyrLys 202
                                                                                                                                          CAAGGCTTCCACACCTTCAGTCTCCATGAGCTGACGGCGATGACGCAGCACCAGCACGAG
                                                                                                                                                                                                                      GAGCTGTTTGTGGAGCCGGACAGCAGCAGCTCTGGAGCACAGGAGAGCAGCTGGGACTCCAGC
                                                                                                                                                                                                                                                         GlnSerTyrMetProProAspSerSerSerProGluAsnLysSerLeuGluValSerAsp 162
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                                                                                                                                                                               ThrArgPheHisSerPheSerPheTyrGluLeuLysAsnValThrAsnAsnPheAspGlu 182
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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LUDWIG INSTITUTE FOR CANCER RESEARCH
                                                                                                                                                   Breast, gastric and prostate cancer associated antigens and uses
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3 34		2510	4	-09-462-261-4	42	Ď,
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Query Match: Percent Similarity: Best Local Similarity: Score: Pred. No.: Alignment Scores: ; LENGTH: 833 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-166-350-10 SEQ ID NO 10 TILE REFERENCE: L0461/7051 CURRENT APPLICATION NUMBER: US/09/166,350A CURRENT FILING DATE: 1998-10-05 EARLIER APPLICATION NUMBER: US 09/166,350 EARLIER FILING DATE: 1998-10-05 NUMBER OF SEQ ID NOS: 35 SOFTWARE: FastSEQ for Windows Version 1.31e-127 1169.00 93.21% 92.83% 48.99% Length: Matches: Conservative: Mismatches: Indels: Gaps: 3.0 310

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Sequence 1, Application US/08587889 Patent No. 5654397
                                                                                  APPLICANT: CAO, Zhaodan
APPLICANT: CROSTON, Glenn E.
APPLICANT: GOEDDEL, David V.
TITLE OF INVENTION: INVERTEUVIN-1 REC
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CORRESPONDENCE ADDRESS:
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                                                                                                                                          RECEPTOR-ASSOCIATED E AND BINDING ASSAY
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Best Local Similarity:
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 3590 base pairs
TYPE: nucleic acid
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NAME: OSMAN Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.:
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TELEFAX: (415) 494-8771
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                   GGTTCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCCATCTCCAGCCCCCTTCTTCTACCAA
                                                 -ValGlnAsnLeuGluGlnSerTyrMetProProAspSerSerSerProGluAsnLysSe 157
                                                                                                 CACCTTCCTCTCCCAGCTTTTCCAGGCTCCCAGACCCATTCAGGGCCTGAGCTCGGCCT
                                                                                                                                          gThrLeuMetThrPro------
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                                                                                                                                                                                                                                                                                                                                                          CCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGTGCGCGGGACATCATCACAGCCTG
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                        GGTGTACGAGAGGCTAGAGAAGCTGCAGGCA 1648
                                                                   sValGlnGlnLeuLeuGlnGluMetThrAla 459
                                                                                                                                                CTACAAGAAGCACCTGGACCCCAGGCCCGGGCCCTGCCCACCTGAGCTGGGCCTGGGCCT
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                                                                                                                 GGGCCAGCTGGCTGCTGCCTGCACCGCCGGGCCAAAAGGAGGCCTCCTATGACCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; CLONE: 91220312
US-09-016-434-1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOI
TITLE OF INVENTION: PATHWAY GENE E:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (650) 845-41 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3590 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
LIBRARY: GENBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: HEREWIT CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS: ADDRESSE: INCYTE PHARMACEUTICALS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: li
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CITY: PALO ALTO
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                                                                                                                                  44 GlyAspAspArg-TyrAsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGl
                                                                                                                                                                                                                         24 AspPheIleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSer
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CGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAACCGCAACGCCCGTGTGGCCGA 324
                                         yLysSerProThrSerGluLeuLeuPheAspTrpGlyThrThrAsnCysThrValGlyAs 83
                                                                                                                                                                                  AGT-----GATGGACGCCCTGGAGCCCGCCGACTG---GTGCCAGTTCGCCGCCCT--- 222
                                                                                                                                                                                                                                                                         CCCCGGCGCCCAGCACTTCTTGTACGAGGTGCCGCCCTGGGTCATGTGCCGCCTTCTACAA 174
                                                                                                                                                                                                                                                                                                                  ProlleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSer
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Gaps:
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                                                                                                                                                                                                   oGluAlaLeuArg---GlyGluIleThrProLysSerAspIleTyrSerPheGlyValVa 376
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uLeuLeuAspIleLysGluGluIleGluAspGlu---
                                                                                                                                                                                                                                                                                                                  -GlnThrValMetThrSerArg------IleValGlyThrThrAlaTyrMetAlaPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGTATGCTGTGAAGAGGCTGAAGGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCA
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                                                                                                    LeuLeuGluIleIleThrGlyLeuProAlaValAspGluHis---ArgGluProGlnLe 395
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               Percent Similarity:
Best Local Similarity:
                                                 Score:
                                                                  Pred. No.:
                                                                               Alignment Scores:
                                                                                                                 PCT-US96-09193-1
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                                                                                                                                                                                                           TELEFAX: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: David J. Brezner
REGISTRATION NUMBER: 24,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tularik, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial No.
FILING DATE: JAN 16 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                               TELEPHONE: (415) 494-8700
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CITY: San Francisco
                                                                                                                                                                               TYPE: nucleic acid
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                                                                                                                                            YSerLeuLeuAspArgLeuSerCys---LeuAspGlyThrProProLeuSerTrpHisMe 287
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES
FILE REPERENCE: MNI-161
CURRENT APPLICATION NUMBER: US/09/579,182
CURRENT FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity:
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TYPE: DNA
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                                 TTCCTAAATCCCGATAAATCAAAGTCTCGACGAGGTCCTGAACAGAAGAAG----GAGCTA
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                                      Sequence 10, Application US/09228986
Patent No. 6359198
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
 TITLE OF INVENTION: Compositions Isolated from Plant Cells TITLE OF INVENTION: and Their Use in the Modification of Plant FILE REFERENCE: 11000/1020
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CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 2336
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                                               AAGGCAACTCCTAGCTCGGACGTGTTCAGCTTCGGTGTTCTGCTGTTGGAGGTGGCTTGC
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Patent No. 6359198
GRNERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
APPLICANT: Nieuwenhuizen, Niels
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LENGTH: 3239
TYPE: DNA
ORGANISM: Eucalyptus
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TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT PILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
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ORGANISM: Pinus
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                                                   SerArgIleValGlyThrThrAlaTyrMetAlaProGluAlaLeu---ArgGlyGluIle 364
                                                                                                 GTTGTTGGAGA
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                   ACTGCTGTTCGAGGGACGGTAGGTCACATTGCCCCCAGAATACCTTTCAACGGGACAATCT 1648
                                                                                                                                 LysIleSerAspPheGlyLeuAlaArgAlaSerGluLysPheAlaGlnThrValMetThr 345
                                                                                                                                                                                                                                                                                         CysLysIleAlaGlnGlyAlaAlaAsnGlyIleAsnPheLeuHisGluAsn-----
                                                                                                                                                                                                                                                                                                                                ---GCCTCTTGTCTTAGAGATCATATTAATGGAAAGCTTGCCCTGGACTGGCCTACTCGC
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Best Local Similarity:
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SEQ ID NO 1
LENGTH: 2288
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CURRENT FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (64)..(1851)
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105 ValProLysThrAlaAsnThrLeuProSer------LysGluAla------IleThr
                                                                                                                                     295
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                                                                                                                                                                                                                                                                                                                                                                    235 ATTGAAAAGTATGTAGACCAAGGTAAAAGTGGAACAAGAGAATTACTTTGGTCCTGGGCA 294
                                                                                                                                                                                                                                                                                                                          36 AlaValAlaIleLysLysProSerGlyAspAspArgTyrAsnGlnPheHisIleArgArg
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                                                                                                                                                                                                                                         PheGluAlaLeuLeuGlnThrGlyLysSerProThrSerGluLeuLeuPheAspTrpGly
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                                                                                             ----LeuIleGlnAsnGluPhePheAlaProAlaSerLeuLeuLeuProAspAla 104
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      GTTTTAAATACTCTTGAAAGTACTCAAGCCAGC 1410
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                                        ValGlnGlnLeuLeuGlnGluMetThrAlaSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/09863549; Patent NO. 6576444; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaodan; TITLE OF INVENTION: IRAK3 Polypeptides, Polynucleotides and FILE REFERENCE: T98-019; CURRENT APPLICATION NUMBER: US/09/863,549; CURRENT FILING DATE: 2001-05-22; PRIOR APPLICATION NUMBER: 09/135,232
PRIOR APPLICATION NUMBER: 09/135,232
PRIOR FILING DATE: 1998-08-17; NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
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; LOCATION: (64)..(1851)
US-09-863-549-1
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US-09-863-549-1
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TYPE: DNA
ORGANISM: human
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  TTCCACAAAGACTTCCTA-----
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                                  PheAspGluArgProIleSerValGlyGlyAsnLysMetGlyGluGlyGlyPheGlyVal 199
                                                                                                                       ValSerAspThrArgPheHisSerPheSerPheTyrGluLeuLysAsnValThrAsnAsn 179
                                                                                                                                                                                                     AsnLeuGluGlnSerTyrMetProProAspSerSerSerProGluAsnLysSerLeuGlu
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Gaps:
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Matches:
Conservative:
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RESULT 11
US-09-228-986-4
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
PILE REPERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 2868
                                                                                                                                                                                                                                                                   Sequence 4, Application US/09228986 Patent No. 6359198
                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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||||||||::::|||:::::|||:::::|||||
AGCTTTGGAATTGTAATAATGGAAGTTCTAACAGGATGTAGAGTAGTTAGATGATCCA 1197
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|||||||||||:::|||
ATCCTTTTGGATGATCAGTTTCAACCCAAACTAACTGATTTTGCCATGGCACACTTCCGG 101
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; ORGANISM: Pinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyGluGlyGlyPheGlyValValTyrLysGly----TyrValAsnAsnThrThrValAla
                                                                                                                                                                                   CAACGGGCATTTGACCTTGCACGTTTAGCAAATGATGATGATGTCATGTTGACTTGACTGG
                                                                                                                                                                                                                                                                       TCTTCGGAAAAGACAGACGTATTTGGATATGGAATCATGTTGCTGGAACTTATTACGGGA
                                                                                                                                                                                                                                                                                           IleThrProLysSerAspIleTyrSerPheGlyValValLeuLeuGluIleIleThrGly
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                                                     ---AsnAspAlaAspSerThrSerValGluAlaMetTyrSerValAlaSerGlnCysLeu
                                                                                                 GTTAAAGGCCTACTA-----AAAGAGAGAAGGCTTGATATGCTAGTTGATCCTGATCTT
                                                                                                                                         IleLysGluGluIleGluAspGluGluLysThrIleGluAspTyrIleAspLysLysMet
                                                                                                                                                                                                                  LeuProAlaValAspGluHisArg------GluProGlnLeuLeuAsp---
                                                                                                                                                                                                                                                                                                                                                           ACGACGGCTGTTCGTGGAACCATTGGCCACATAGCACCTGAGTACCTTTCTACTGGAAAG
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Ouery Match:
                                                                                                                                                                                                                                                                 US-10-001-254-16 (1-460) x US-08-447-185-2 (1-966)
                                                                                                                                                                                                                                                                                                     DB:
                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores: Pred. No.:
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US-08-447-185-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5648599
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (716)-263-16 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Goldman Mr., Michael
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tanksley, Steven D.

APPLICANT: Martin, Gregory B.

TITLE OF INVENTION: GENE CONFERRING DISEASE RESISTANCE
TITLE OF INVENTION: TO PLANTS BY RESPONDING TO AN AVIRULENCE GENE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                            Sequence 3, Application Patent No. 5648599
                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Tanksley, Steven D.
APPLICANT: Martin, Gregory B.
TITLE OF INVENTION: GENE CONFERRING DISEASE
TITLE OF INVENTION: TO PLANTS BY RESPONDING
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                               CORRESPONDENCE ADDRESS:
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CITY: R
                                                                COUNTRY:
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                                                                                                               Clinton Square,
                                                                  U.S.A.
                                                                                                                                 Michael L. Goldman
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TELEFAX: (716)-263-1600
; INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2443 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-447-185-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/447,185
FILING DATE:
CLASSIFICATION BOD
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/111,078
FILING DATE:
APPLICATION NUMBER: US/08/111,078
FILING DATE:
APPLICATION NUMBER: US/08/111,078
FILING DATE:
APPLICATION HOPERATION:
TELEPHONE: (716)263-1000
TELEPHONE: (716)263-1000
                                    316
                                                                           805
                                                                                                             296
                                                                                                                                                448 TCAGATCTACCCACAATGAGCATGAGCTGGGAGCAGAGCTGGAGATATGCATAGGGGCA
                                                                                                                                                                                 277 LeuAsp---GlyThrProProLeuSerTrpHisMetArgCysLysIleAlaGlnGlyAla 295
                                                                                                                                                                                                                             388
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                                                                                                                                                                                                                                                                                                                                                                            274
                                                                                                                                                                                                                                                                                                                                                                                                   220 AspIleThrThrGluGluLeuLysGln------GlnPheAspGlnGluIleLysVal 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                     229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 GÄTCACAAGTTTTTA------ATTGGÄCATGGTGTCTTTGGGAAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AspGluArgProIleSerValGlyGlyAsnLysMetGlyGluGlyGlyPheGlyValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142
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                                                                                                                                                                                                                                                257 AspLeuCysLeuValTyrValTyrMetProAsnGlySerLeuLeuAspArgLeuSerCys 276
                                                                                                                                                                                                                                                                                                                                     237 MetAlaLysCysGlnHisGluAsnLeuValGluLeuLeuGlyPheSerSerAspGlyAsp 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 TyrLysGlyTyrVal---AsnAsnThrThrValAlaValLysLysLeuAlaAlaMetVal 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 SerAspThrArgPheHisSerPheSerPheTyrGluLeuLysAsnValThrAsnAsnPhe 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 LeuGluGlnSerTyrMetProProAspSerSerSerProGluAsnLysSerLeuGluVal 160
ASNIIeLeuLeuAspGluAlaPheThrAlaLysIleSerAspPheGlyLeuAlaArgAla 335
                                                                         GCCAGAGGTCTACACTACCTTCATACTAGAGCAATTATACATCGTGATGTCAAGTCTATA
                                                                                                         AlaAsnGlyIleAsnPheLeuHisGluAsnHisHisIleHisArgAspIleLysSerAla 315
                                                                                                                                                                                                                         GAGATGATTCTAATTTATAAATACATGGAAGATGGGAACCTCAAGAGACATTTGTATGGA 447
                                                                                                                                                                                                                                                                                                                                                                        -----CGTACACCTGAGTCCTCACAAGGTATTGAAGAGTTCGAAACAGAAATTGAGACT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACAAGGGTGTTTTGCGTGATGGAGCAAAGGTGGCCCTGAAAAAGG------
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430.50
49.55%
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Alignment S Pred. No.: Score: Percent Sim	RESULT 14 US-07-717-331F- Sequence 4, A Patent NO. 54 PAPLICANT: PAPLICANT: PAPLICANT: PAPLICANT: COUNTRY: COUNTRY: ZIP: 06 COMPUTER R COMPUTER R PAPLICAT COMPUTER R PAPLICAT PILING D APPLICAT PILICOMMUN SEGUENCE C LENGTH: INFORMATION SEQUENCE C INFORMATION SEQUENCE C INFORMATION SEQUENCE C JENGTH: JYPE: n STRANDED JENGTH: JYPE: n JYPE:	Qy 4 Db 9	Qy 4	Qy 3	Qy 3	Qy 3	Qy 3	DB 60
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9.43e-40 427.50 44.25%	17331 Mich Mich Mich 2	CysLeuHisGluLysLysAsnLysArgP 	.snAspAlaAspSerThrSerValGluAlaMe 	BGluGluIleGluAspGlu ::: -GAACAAATCGTAGATCCC	Ala TAGCTGAATGGGCA	JeuGlu TTCGAAGTTCTTTGT	AlaLeuArgGlyGluIleThr ::::: :ATTTTATAAAGGGACGACTCACT	heAlaGlnThrVal TTGATCAAACCCAT
Length: Matches: Conservative:	el Nasrallah; rotein Kinase ne Self-Incomp	LeuHisGluLysLysAsnLysArgProAspIleLysLysVa 	.GluAlaMetTyr ::::: \GAGTCCCTCAGGAA	GluLysThrIleGl	AlaValAspGluHisArgGluProGlnLeu :: ATGGTTAATTTAGCTGAATGGGCAGTGGAGTCGCATAATAATGGACAGTTG	GCTAGGTCTGCCAT	GluIleThrProLy	MetThrSerArgIl: :::::::::::::::::::::::::::::::::::
2749 152 75	and Joshua Gene atability Locus	BLysVal 450 TGATGTG 981	AsnAspAlaAspSerThrSerValGluAlaMetTyrSerValAlaSerGln 	pGluGluLysThrIleGluAspTyrIleAspLysLys TCCC	AlaValAspGluHisArgGluProGlnLeuLeuLeuAs :: GCAGTGGAGTCGCATAATAATGGACAGTTG	ValValLeuLeuGlu	AlaProGluAlaLeuArgGlyGluIleThrProLysSerAspIleTyrSerPheGly	SerGluLysPheAlaGlnThrValMetThrSerArgIleValGlyThrThrAlaTyrMet ::::
			rGln 435 ::: AAAA 936	sMet 418	μAsp 398	385 GAG 807	Gly 374	Met 355 ::: CATT 687

Q Q D .	Q B Q B Q B Q B	8 8 8 8 8 8 8	P	Best I Query DB: US-10- Qy Db Qy Db Qy Db
CTTGTCCGACTTCTTGGCTGTTGTGTTTATGAGGGCGAGAAGATCTTAATTTACGAGTAC Met ProAsnGlySerLeuLeuAspArgLeuSerCysLeuAspGly :::	186 SerValGlyGlyAsnLysmetGlyGluGlyGlyPheGlyValValTyrLysGlyTyr 204 186 SerValGlyGlyAsnLysmetGlyGluGlyGlyPheGlyValValTyrLysGlyTyr 204 1609TTTAACAAGGTCGGAAAAGGTGGTTTTGGTGTTTTACAAGGGAAGGTTA 1659 205 ValAsnAsnThrThrValAlaValLysLysLeuAlaAlaMetValAspIleThrThrGlu 224	106 ProLysThrAlaAsnThrLeuProSerLysGluAlaIleThrValGlnGlnLysGlnMet 125	SerGlyAspAspArgTyrAsnGlnPheHis	Best Local Similarity: 29.63% Nismatches: 157 Query Match: 17.92% Indels: 129 DB: 129 US-10-001-254-16 (1-460) x US-07-717-331F-4 (1-2749) Qy 1 MetAsnLysbrolleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIle 19
SIFICATION EY/AGENT : STEFFE; STRATION N RENCE/DOCI MMUNICATION PHONE: (20) FFAX: (20) FFAX: (20) CE CHARACT	CORRESPITING SCHUENCES: 14 CORRESPONDENCE ADDRESS: ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600 CITY: WASHINGTON STATE: D.C. COUNTRY: USA ZIP: 2005-3934 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/980,060 FILING DATE: Herewith	THE C E-0	Db 2173 TTGCTTCTTGAAATTATAAGTGGCAAGAGGAACAAAGGC 2211 Oy 396 LeuLeuAspIleLysGluGluIleGlu	300 AsnPheLeuHisGluAsnHisHis

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TYPE: nucleic acid
STRANDENESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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LOCATION:
   270
                                                       250 GlyPheSerSerAspGlyAspAspLeuCysLeuValTyrValTyrMetProAsnGlySer 269
                                                                                                       793
                                                                                                                                                                                                                                                                   190 AsnLysMetGlyGluGlyGlyPheGlyValValTyrLysGlyTyrValAsnAsnThrThr 209
                                                                                                                                                                                                                                                                                                                                                                                   571 ACCTCCATTCCTAAGCAGGAAAAACTTTTGAGCTTGGCTGGAGACAGCCTTTTCTGGAGT 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                  511 GATGCCCTCATTCCTTGAGAAGCGACCTCCCCACTTCGTCTGATTCAAAGGACTTCAGC 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       451 GGCCCAGGGTCCTCCAGCCAGAGCCCACCAGCCGGCCTTTCTCCAGCCTCCTGAAGAA 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397 AAGGCTGAGGATGAACAGGAAGAGGGGCAGCCTGTG-----AGGATGGCCACCTTTCCA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337 CCCATTCCAGCCTTCCCTGACTCTGTGAAGCCAGAAAAGCCTTTGGCAGCTTCTGTAAGA 396
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                                                                                                                                    230 PheAspGlnGluIleLysValMetAlaLysCysGlnHisGluAsnLeuValGluLeuLeu 249
                                                                                                                                                                                                         210 ValAlaValLysLysLeuAlaAlaMetValAspIleThrThrGluGluLeuLysGlnGln 229
                                                                                                                                                                                                                                                                                                               631 GAGGCAGACGTGGTCCAGGCAACCGATGACTTCAATCAA------AAC 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 GluAlaIleThrValGlnGlnLysGlnMetProPheCysAspLysAspArgThrLeuMet 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 TGGTGGTGGGGCATGCGGCAGGCCACCGTCCAGCAACTTGTGGACCTCCTGTGCCGCCTG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 GluPhePheAlaProAlaSerLeuLeuLeu----- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 IleArgArgPheGluAlaLeuLeuGlnThr---GlyLysSerProThrSerGluLeuLeu
LeuLeuAspArgLeuSerCysLeuAspGlyThrProProLeuSerTrpHisMetArgCys 289
                                 GGCTTCTGTGCTGCAAGACAGTTTCACAGCTTCATCTACCCCTACATGGCAAATGGTTCC
                                                                                                     TTCCAGGCAGAGTTGCAGATTTGTCTTAGATGCTGCCACCCCAATGTCTTACCTGTGCTG 852
                                                                                                                                                                       TTCGTCTTCAAGAAGCTCAGAGAGACAGCCTGTTCAAGTCCAGGATCAATCGAAAGATTC 792
                                                                                                                                                                                                                                           CGCAAAATCAGCCAGGGACCTTTGCTGACGTCTACAGAGGGCACAGGCACGGGAAGCCA 732
                                                                                                                                                                                                                                                                                                                                   PheTyrGluLeuLysAsnValThrAsnAsnPheAspGluArgProIleSerValGlyGly 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerSerProGluAsnLysSerLeuGluVal------SerAspThrArgPheHisSer 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ProAspAlaVal---ProLysThrAlaAsnThrLeuProSerLys 115
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1498CTGCAGAAGTGTGTGTCT 1518	449 LysValGlnGlnLeuLeuGlnGluMetThrAlaSer 460	1453 CTGGCCACGGCTGCCTGTGCCTGCGGAGGCGTAACACCAGC 1497	429 MetTyrSerValAlaSerGlnCysLeuHisGluLysLysAsnLysArgProAspIleLys 448	1393 ATCTGCCAGAAGTACCTGGAGAAAGGGCGCAGGGAGGCTTCCGGAGGACTGCGCCGAGGCC 1452	409 ThrileGluAspTyrTleAspLysLysMetAsnAspAlaAspSerThrSerValGluAla 428 	1333 AGCAGCACCGCCTCGCTCCCAGGAAGACGGGCGTGGAGAACGTGATGGCAAAGGAG 1392	400GluGluLys 408	1273 GCAATGGATAACAACCGAAGCCCGGTTTACCTGAAGGACTTACTCCTCAGTGAAATTCCA 1332	386 AlaValAspGluHisArgGluProGlnLeuLeuLeuAspIle	1213 AAGCGAGTGGACATCTTCAGCTGTGGAATAGTGTTGGCCGAGGTCCTCACGGGCATCCCT 1272	366 ProLysSerAsplleTyrSerPheGlyValValLeuLeuGluIleIleThrGlyLeuPro 385	1153 CTGCTCCGGACGTCAGCCGCGTATCTGCCAGAGGATTTCATCCGGGTGGGGCAGGTGACA 1212	348 IleValGlyThrThrAlaTyrMetAlaProGluAlaLeuArgGlyGluIleThr 365	1093 CCAATGGCTCATCTGTGTCCTGTCAACAAAAGGTCAAAATACACCATGATGAAGACTCAC 1152	330PheGlyLeuAlaArgAlaSerGluLysPheAlaGlnThrValMetThrSerArg 347	1033 AGCAACGTCAAGAGCTCTAATGTCTTGCTGGACCAAAATCTCACCCCCAAACTTGCTCAC 1092	310 ArgAspīleLysSerAlaAsnīleLeuLeuAspGluAlaPheThrAlaLysIleSerAsp 329	973 AGCATCTGCTCAGGGCTGCTCTGTGCCGTCGAGTACCTGCATGGTCTGGAGATCATCCAC 1032	290 LysileAlaGlnGlyAlaAlaAsnGlyIleAsnPheLeuHisGluAsnHisHisIleHis 309	

Search completed: January 18, 2004, 06:10:41 Job time: 145.032 secs

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Result
No.
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-Q=/Ggn2 | /USPTO_spool/USI01001254/runat 16012004 152426 19815/app_query.fasta_1.1109
-DB=Published_Applications_NA_QFWT=fastap_SUFFIX=rnpb_MINMATCH=0.1
-LOOPELT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US10001254 @CGN 1 1 534 @runat 16012004 152426 19815
-NCPU=5 -ICPU=3 -NO_MAND -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOD=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 200000000
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Listing first 45 summaries
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Perfect score:
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-MODEL=frame+_p2n.model -DEV=xlh
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                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
      Score
Query
Match Length DB
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| Cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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| Cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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                                                                                                  SUMMARIES
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ALIGNMENTS

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RESULT 1

US-10-001-254-15

US-10-001-254-15

Sequence 15, Application US/10001254

; Publication No. US20030049702A1

; GENERAL INFORMATION:

; APPLICANT: Reed, John C.

; APPLICANT: Pawlowski, Krzysztof

APPLICANT: Powlowski, Krzysztof

; APPLICANT: Powlowski, Krzysztof

; APPLICANT: Powlowski, Krzysztof

; APPLICANT: Roth, Wilfred

; APPLICANT: Roth, Wilfred

; APPLICANT: Stenner-Liewen, Frank

; TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins

; FILE REFERENCE: P-LJ 5037

; CURRENT APPLICATION NUMBER: 05/30/1,254

; CURRENT APPLICATION NUMBER: 05/30/1,889

PRIOR APPLICATION NUMBER: 09/715,893

; PRIOR APPLICATION NUMBER: 09/715,893

; PRIOR FILING DATE: 2001-10-29

; PRIOR FILING DATE: 2000-11-17

; NUMBER OF SEQ ID NOS: 62

; SEQ ID NO 15

; SEQ ID NO 15

; LENGTH: 1383
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Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; RAME/KEY: CDS
; LOCATION: (1)...(1380)
US-10-001-254-15
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                      IleThrThrGluGluLeuLysGlnGlnPheAspGlnGluIleLysValMetAlaLysCys
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                                                                                                                                                                                                                                                                                                            MetAsnLysProIleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg
                                                                          TyrLysGlyTyrValAsnAsnThrThrValAlaValLysLysLeuAlaAlaMetValAsp
                                                                    TATAAAGGCTACGTAAATAACACAACTGTGGCAGTGAAGAAGCTTGCAGCAATGGTTGAC
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Align Pred. Score Perce Best Query DB:	RESULUS -09 Sequence GEN AP AP FII CCU CCU CCU NUM NUM FR CCU CCU CCU CCU CCU CCU CCU	B 8	B 8	B &	B &	B 8	B 8	B &	Db	Q	B 2	5
Alignment Scores: 1.06e-258 Length: 1383 Pred. No.: 2382.00 Matches: 459 Score: 2382.00 Matches: 0 Percent Similarity: 99.78\$ Conservative: 0 Best Local Similarity: 99.78\$ Mismatches: 1 Query Match: 99.83\$ Indels: 0 DB: Gaps: 0	ps-595-2 pstion No. US20030059916A1 LINFORMATION: LLINFORMATION: LLINFORMATION: LLINFORMATION: LLINFORMATION: CANT: Li, Shyun COANT: Tilarik Inc. COANT: Tilarik Inc. COANT: Tilarik Inc. COANT: TILING DATE: 2001-01-13 R FILING DATE: 2001-01-13 R OF SEQ ID NOS: 7 PARE: Patentin Ver. 2.1 NO 2 PTH: 1383 BINA NISM: Homo sapiens TURE: R INFORMATION: human IL-1 receptor-associated kinase 4 RR INFORMATION: cDNA TURE: CDS NYION: (1)(1383) RR INFORMATION: human IRAK-4 S9-595-2	441 LysasnLysargProaspIleLysLysValGlnGlnLeuLeuGlnGluMet. 	Qy 421 AlaAspSerThrSerValGluAlaMetTyrSerValAlaSerGlnCysLeuHi 	401 GluGluIleGluAspGluGluLysThrIleGluAspTyrIleAspLysLy 	381 IleThrGlyLeuProAlaValAspGluHisArgGluPi 	361 ArgGlyGluIleThrProLysSerAspIleTyrSerPheGlyValValLe	341 GlnThrValMetThrSerArgIleValGlyThrThrAlaTyrMetAlaJ 	Qy 321 GluAlaPheThrAlaLysIleSerAspPheGlyLeuAlaArgAlaSerGluLysPheA	901 TTTCTACATGAAAATCATCATATTCATAGAGATATT	301 F	841	281 F
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-10-001-254-16 (1-460) x US-09-759-595-2 (1-1383)
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| Publication No. US20030087856A1
| GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: C. Frank Bennett APPLICANT: SUSAN M. Freier
| TITLE OF INVENTION: ANTISENSE MODULATION OF IL-
| FILE REFERENCE: RTS-0324
| CURRENT APPLICATION NUMBER: US/09/966,451
| CURRENT FILING DATE: 2001-09-28
| NUMBER OF SEQ ID NOS: 88
| SEQ ID NO 3
| LENGTH: 2817
| Type: DNA
| ORGANISM: Homo sapiens
| FEATURE: NAME/KEY: CDS | LOCATION: (50)...(1432)
| US-09-966-451-3
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                                          ValGlyAspLeuValAspLeuLeuIleGlnAsnGluPhePheAlaProAlaSerLeuLeu
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                                                                                                                                             LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLys
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                            GTTGGTGATCTTGTGGATCTTTTGATCCAAAATGAATTTTTTTGCTCCTGCGAGTCTTTTG
                                                                                     CAAACTGGAAAAAGTCCCCACTTCTGAATTACTGTTTGACTGGGGCACCACAAATTGCACA
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Publication No. US20030049702A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
APPLICANT: Fiorentino, Loredana
APPLICANT: Fiorentino, Loredana
APPLICANT: Lee, Sug Hyung
APPLICANT: Lee, Sug Hyung
APPLICANT: Roth, Wilfred
APPLICANT: Roth, Wilfred
APPLICANT: Roth, Wilfred
APPLICANT: Roth, Wilfred
APPLICANT: No. US2003004970ZA1el Death Dom
FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT APPLICATION NUMBER: 60/301,889
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 27
LENGTH: 2817
TYPE: DNA
ORGANISM: Homo sapien
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SerAspThrArgPheHisSerPheSerPheTyrGluLeuLysAsnValThrAsnAsnPhe
                                                            LeuGluGlnSerTyrMetProProAspSerSerSerProGluAsnLysSerLeuGluVal
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RESULT 5
US-09-759-59-4

(Sequence 4, Application US/09759595

(Publication No. US20030059916A1)

(GENERAL INFORMATION:
APPLICANT: Wesche, Holger
APPLICANT: Li, Shyun
APPLICANT: Tularik Inc.

(TITLE OF INVENTION: IRAK-4: Compositions and
FILE REFERENCE: 0.18781-003910US

(CURRENT APPLICATION NUMBER: US/09/759,595

(CURRENT FILING DATE: 2000-01-13

PRIOR APPLICATION NUMBER: US 60/176,395

PRIOR APPLICATION STEP 100-01-13

PRIOR APPLICATION NUMBER: US 60/176,395

PRIOR APPLICATION NUMBER: US 60/176,395
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DB:
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SEQ ID NO 4
LENGTH: 1542
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ORGANISM: MUB Sp.
FEATURE:
OTHER INFORMATION: murin-
OTHER INFORMATION: cDNA
FEATURE:
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                                             IleThrThrGluGuLeuLysGlnGlnPheAspGlnGluIleLysValMetAlaLysCys
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US-09-764-868-249
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                              US-10-001-254-16 (1-460) x US-09-764-868-249 (1-1493)
                                                                                                                                                                                                                                                                                                                     Sequence 249, Application US/09764868
Patent NO. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                            Prior application data removed -
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 249
LENGTH: 1493
TYPE: DNA
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             SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                          ZIP: 02140
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
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                                                                                                                                                                                                                STATE: MA
NAME: Sprunger,
                                                                                                                                                                                              COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                         McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa
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REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:

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US-09-833-790-149
; Sequence 149, Application US/09833790
; Patent No. US2002068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tongtong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Indirias, Carol Y.
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Best Local Similarity:
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TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
         APPLICANT: Fan, Liq
TITLE OF INVENTION:
TITLE OF INVENTION:
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INVENTION: COMPOSITIONS AND METHODS FOR THE
INVENTION: AND DIAGNOSIS OF LUNG CANCER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc feat
; LOCATION: (1)...(50
; OTHER INFORMATION:
US-09-833-790-149
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                                                                                                   Sequence 10, Application US/09966451 Publication No. US20030087856A1 GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FAStSEQ for Windows Version 4.0
SEQ ID NO 149
LENGTH: 501
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION
FILE REFERENCE: RTS-0324
CURRENT FILLING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 88
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ORGANISM: Homo :
FEATURE:
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DD 13743 TUTUTTIACUCATUTTUATTATAAUTTAGAGATTUTTAGGGAAGUTTUTTUTTUTTUTTUTTUTTUTTUTTUTTUTTUTTUTT		102	GTGCTTCAGTGCCTCTGATATAGGTGGCTCATGGATCACTGTTTGAAAACACTGCCTTAC 1	100	13623 GTTCCAAATCTATGTAATCAGAATTCTGGAATTGGGTTTAAGGTCTATATTCTTAAACAG 1	Qy 102 102	Db 13563 ACCTTTATCATGCATAAGAATCACTTAGGTTCTGGTTAAACATGTAGTTTCCTAGGGTCT 13622	Qy 102 102	Db 13503 GTTGCCTTATAAGCTTTCTTTTTTTCCTTTGATGCCTTTCACACCAGTGGTTCTCA 13562	Qy 102 102	Db 13443 CCCTGATGGGACTCTATAATCATAATTTTAAAAAATTGTATTCTGATGTGGTAGTGTCTA 13502	102	13383 TAGGCTGTAAGAAAGTAATTATAATTTGAGTTCTTCCCTTTTTTTGATCTTCAACTTCTA 1	102	27 - TO TO THE TOTAL THE TOTAL AND THE TOTAL AND THE TOTAL AND THE TOTAL THE TOTAL AND	13263 AAAAGCAGCACAGACAAAGGACACIGIGGACICIGGIGCIAAGGIGAIAGAAGCIICGIA 1		100	1 3203 TCATAGTAGATGAAGCTTACATTTGAGAGTCCCTTTTCTTGAGCACTCCTCCAACTCCTTTA 1	102	13143 ATTAGGGTGGAAAGACAAATGGCAGAAATATAAATGTTTCTTCTTACTCTTTCTT	Qy 102 102	13083 TTTTTTGCTCCTGCGAGTCTTTTTGCTCCCAGGTAAACTGATTGTGACCAGGGTGTCCACA 1	93 PhePheAlaProAlaSerLeuLeuPro93	Qy 73 AspTrpGlyThrThrAsnCysThrValGlyAspLeuValAspLeuLeuIleGlnAsnGlu 92	Db 12963 TTAÁGGAGAÍTTIGAÁGCÁTTACTTCAÁACTGGAAAÁGTCCCACTTCTGAÁTTÁCTGTTT 13022	gPheGluAlaLeuLeuGlnThrGlyLysSerF	US-10-001-254-16 (1-460) x US-09-966-451-10 (1-31000)	24.73% 11	26.94% Conservative: 4	2.44e-54 Length: 590.00 Matches:	1 in a section of the	TIS-09-966-451-10	
RESULT 10	Db 14823 AAGTTATATTTCAGGAATAAAAGAAAGAG 14853	tValAspIleThrThrGluGluLeuLysGln 228	Db 14763 AGTTGTATATAAAGGCTACGTAAATAACACAACTGTGGCAGTGAAGAAGCTTGCAGCAGT 14822	Qy 198 yValValTyrLysGlyTyrValAsnAsnThrThrValAlaValLysLysLeuAlaAlaMe 218		nAsnPheAspGluArgProIleSerValGlyGlyAsnLysMetGlyGlyGlyGlyPhGG1 198	14643 TICTIATITIQACATAWGITITICACAGITITICATITIATIQAATIQAAGAATQICACAGAA 1470		14303 AICIIVAMAIDASAAANIAIIAIAAAIIAIIAAAANVOAAIIIIIAAAAAAIIIAAAAAAIIIAAAAAAIIIAAAAAA	ן איין איין אַ מַנְאָרְאָרְאָרְאָרְאָרְאָרְאָרְאָרְאָרְאָר	14523 TEGITTTAICTTCICICATCITISICIMALICAMAAICAIMAAAAIIIIGCAIAAAAIGIGAA 150	164 16	Db 14463 CAGAGGGTAGGATCACCAAACAGAGTTCTCAAGAAAAACTTATAATTTGTATTTTAGAAA 14522	Qy 164 164	Db 14403 TAGGTAGACTAGACCCACTCAAATGTGTGACTAGAATTTTGGGTGGG	Qy 164 164	Db 14343 ATATTTACATAACTTGGAAAGGTCACTTTTTAAAATAAAT	Qy 164 164	Db 14283 AGTGATTAGAGGCAATAGGACATGCAAACCAGCAGAGAAGCTATGAAAAAAAA	164	Db 14223 TAGCTCTTTTGTGAGTTGTTTCCTCCTGATATAATAAGAACCATCTTCATTGTATTAATC 14282	164	14163 GTGCTTTAAAAGAAAGCTCTTGCTCTTTTGTTTTGTGCAGCAATCACAGGCACACTGGCAA 14	Qy 164 164		161	Qy 141 ugluGinserTyrMetPrOPrOAspSerSerVeTPrOSUMASHLYSSerLeuginvalse isi	13783 GEMANANCHURAIGEE11161GANCHANNANCHURANANCHURANANCHURANCHURANANCHURANANCH 1887			Qy 103AspAlaValProLysThrAlaAsnThrLeuProSerLysGluAlaIleThrValG1 121	Db 13863 GTTTAACTTTTTCACAACCACTTTTTCTTACTGAAAAACCACTTGTATCTTACTTCATTT 13922	Qy 102 102	THE TRANSPORT TO THE TRANSPORT OF THE TRANSPORT TO THE TRANSPORT OF THE TR

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RESULT 11
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                                                                                                                                          Sequence 2222, Application US/09880107 Patent No. US20020142981A1 GENERAL INFORMATION:
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APPLICANT: Godzik
APPLICANT: Pawlow
APPLICANT: Fioren
APPLICANT: Lee, S
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Publication No. US20030049702A1
APPLICANT: Horne, Darci T.
APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
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TITLE OF INVENTION: No. US20030049702A1el Death
FILE REFERENCE: P-LJ 5037
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LOCATION: (1)...
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                                                                                                                                                                                                                                               ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
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PRIOR FILLING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILLING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                    113
 208 rThrValAlaValLysLysLeuAlaAlaMetValAspIleThrThrGluGluLeuLysGl
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                                    ----CTCAAGATCGGGGAGGGTGGCTTTGGGTGCGTGTACCGGGCGGTGATGAGGAACAC
                                                           yGlyAsnLysMetGlyGluGlyGlyPheGlyValValTyrLysGlyTyrValAsnAsnTh
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                                                                                                        GCCCCTCTGTGAGATTTCCCGGGGCACCCACAACTTCTCGGAGGAG
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                                                                                                                                     eSerPheTyrGluLeuLysAsnValThrAsnAsnPheAspGluArgProIleSerValGl
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; Sequence 4, Application US/10167034
; Publication No. US20030228690A1
; GENERAL INFORMATION:
   APPLICANT: Brenda F. Baker
   APPLICANT: Susan M. Freier
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTIENSE MODULATION OF IL.
; FILE REFERENCE: PTS-0003
; CURRENT APPLICATION NUMBER: US/10/167,034
; CURRENT FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 142
; SEQ ID NO 4
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   nGlnPheAspGlnGluIleLysValMetAlaLysCysGlnHisGluAsnLeuValGluLe
                                                       GGTGTATGCTGTGAAGAGGCTGAAGGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCA
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                                                                                                                   ----CTCAAGATCGGGGAGGGTGGCTTTGGGTGCTGTACCGGGCGGTGATGAGGAACAC
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APPLICANT: WAN, JACKSON
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND MET
FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR PILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 88
LENGTH: 3590
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-10-101-510-88
                                                                                                                                                                                                                                                                             Sequence 88, Application US/10101510 Publication No. US20030148295A1 GENERAL INFORMATION:
      ORGANISM: Homo sapiens
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ySerLeuLeuAspArgLeuSerCys---LeuAspGlyThrProProLeuSerTrpHisMe
                                      TGCTGGCTACTGTGCTCAGAACGGCTTCTACTGCCTGGTGTACGGCTTCCTGCCCAACGG
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                                   GAGCTTCCTGACCGAGGTGGAGCAGCTGTCCAGGTTTCGTCACCCAAACATTGTGGACTT
                                                              nGlnPheAspGlnGluIleLysValMetAlaLysCysGlnHisGluAsnLeuValGluLe
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                                                                                               GGTGTATGCTGTGAAGAGGCTGAAGGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCA
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APPLICANT: Harper, Jeff
APPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLA
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEG ID NOS: 5379
SEQ ID NO 1673
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 AspGluGluLysThrIleGluAspTyrIleAspLysLysMetAsnAspAla---AspSer 423
                                                        ATAATTCAGCAATCTCGTGAAAAGCCTCACCTAGTAGAATGGGTTGGATTTATTGTAAGA
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Search Job ti	Ъ	Ş	Db	8	DЪ
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Search completed: January 18, 2004, 09:06:01 Job time : 721.136 secs	2212 AGACCAAGCATGTCTCAAGTTGTTAGCGATCTTAAAGAGTGTGTGATATCT 2262	444 ArgProAspIleLysLysValGlnGlnLeuLeuGlnGluMetThrAlaSer 460	2152 GGTTCTGTCTGGAAGGCTATTGAACTAGCTATGTCATGTGTGAATATTTCTTCGGCAAGA 2211	424 ThrSerValGluAlaMetTyrSerValAlaSerGlnCysLeuHisGluLysLysAsnLys 443	2098 ACGGGAGATATTGGAAATATTGTTGATCCAAACCTTCACGGAGCTTACGACGTC 2151

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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q-/cgn2_1/USPTQ_spool/US10001254/runat 16012004_152424_19723/app_query.fasta_1.1109
-Q-/cgn2_1/USPTQ_spool/US10001254/runat 16012004_152424_19723/app_query.fasta_1.1109
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosun62 -TRANS=human10.cdi -LIST=45
-DCCALICM=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALICM=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=200000000
-USER=US10001254 @CGN 1 1 4382 @runat 16012004 152424 19723 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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DEFINITION
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KEYWORDS
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ORGANISM

AK028837

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Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)
6 (bases 1 to 2481)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
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Best Local Similarity:
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                                                                                                                                                                                                                                          41 LysProSerGlyAspAspArgTyrAsnGlnPheHisIleArgArgPheGluAlaLeuLeu
                                            81 ValGlyAspLeuValAspLeuLeuIleGlnAsnGluPhePheAlaProAlaSerLeuLeu
                                                                                                                                                   61 GlnThrGlyLysSerProThrSerGluLeuLeuPheAspTrpGlyThrThrAsnCysThr
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Encyclopedia Project of Genome Exploration Research Group in Rike
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
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Please visit our web site for further details.
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DDRYNOPHIRREALLOTGKSPTCELLFDWGTTNCTVGDLVDLVQIELFAPATLLLF
DAVPQTVKSLFPREAATVAQTHGPCOEKDRTSVMPMPKLEHSCEPPDSSSPDNRSVES
SDTRFHSFSFHELKSITNNFDEQPASAGGNRMGEGGFGVVYKGCVNNTIVAVKKLGAM
VRISTEELKQQFDQEIKVMATCQHENLVELLGFSSDSDNLCLVYAXMEPMGSLLDRLSC
LDGTPPLSWHTRCKVAQGTANGIRFLHENHHIHRDIKSANILLDKDFTAKISDFGLAR
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receptor-associated kinase 4 [Mus musculus]
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/tissue type="skin"
/clone_Tib="RIKEN full-length enriched mouse cDNA library"
/dev stage="10 days neonate"
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                                  LysAsnLysArgProAspIleLysLysValGlnGlnLeuLeuGlnGluMetThrAla
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional of 60,770 full-length cDNAs

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2810)

Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Bono,H.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,I

Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hira
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                                                                                                                                                                                                  The FANTOM Consortium and the Group Phase I & II Team.
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC) RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoh Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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                        ValGlyAspLeuValAspLeuLeuIleGlnAsnGluPhePheAlaProAlaSerLeuLeu
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BG164491 BG164491.1 GI:12671194 EST.
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10240 row: d column: 08
High quality sequence stop: 634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                    GlnThrGlyLysSerProThrSerGluLeuLeuPheAspTrpGlyThrThrAsnCysThr
                  ValGlyAspLeuValAspLeuLeuIleGlnAsnGluPhePheAlaProAlaSerLeuLeu 100
                                                                                                                                                             LysProSerGlyAspAspArgTyrAsnGlnPheHislleArgArgPheGluAlaLeuLeu
                                                                                                                                                                                                                             LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLys
                                                                                                                                                                                                                                                                                                 MetAsnLysProIleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg
                                                                                                                                                                                                         AAGCTGTCAGATTTTATTGATCCTCAAGAAGGATGGAAGAAGTTAGCTGTAGCTATTAAA
                                                                                                                                                                                                                                                                             ATGAACAAACCCATAACACCATCAACATATGTGCGCTGCCTCAATGTTGGACTAATTAGG
                                                                                                                                     AAACCATCTGGTGATGATAGATACAATCAGTTTCACATAAGGAGATTTGAAGCATTACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:4452055"
/tissue_type="hypernephroma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_89"
/clone_lib="NIH_MGC_89"
/note="Organ: kIdney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT_primed.
Site_2: SalI; Cloned unidirectionally; oligo-dT_primed.
Average innert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC_Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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RESULT 4
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http://image.llnl.gov
Plate: LLCM1063 row: k column:
High quality sequence stop: 617.
Location/Qualifiers
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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/lab_host="DHIOB (T1 phage-resistant)"
/clone lib="NHH MGC 81"
/note="Torgan; muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site_1: Sfil (ggccgcctcggcc); Site_2: Sfil
(ggccattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                                                                                                                                                               clone="IMAGE:4247171"
                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
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BASE COUNT ORIGIN

222

119 c

142 g

198 t

1 others

C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

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RESULT 5
BQ780493/c
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                                                                                                                                                               uAlaPheThrAlaLysIleSerAspPhe-GlyLeu-AlaArgAlaSerGluLysPheAla
                                                                                                                                                                                                                                                                                                            eThrThrGluGluLeuLysGlnGlnPheAspGlnGluIleLysValMetAlaLysCysGl
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                                                CGTGGAGAAATTAAACCAAA-TCTGATATTAACAGGTTGGGG
                                                                                                                                                                                                              eLeuHisGluAsnHisHisIleHisArgAspIleLysSerAlaAsnIleLeuLeuAspGl
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UI-R-FF0-coz-d-10-0-UI.sl UI-R-FF0 Rattus norvegicus cDNA clone UI-R-FF0-coz-d-10-0-UI 3', mRNA sequence. BQ780493.1 GI:21988965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Jeff Stevens cDNA Library preparation: Dr. M. Bento Soares, University of IovacDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: DISTRIBUTION: Researchers may obtain clones from Research Genetics (www.resgen.com).
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Bonaldo, M.F., Lenno
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Fax: 319 335 9565
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375 Newton Road , 4156
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Coordinated Laboratory
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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TAG_TISSUE=cartilage
TAG_SEQ=CTAATGGACG"
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/mal_type="mRNA"
/mal_type="mRNA"
/db xref="taxon:10116"
/clone="UI-R-FF0-coz-d-10-0-UI"
/tlssue type="Mixed tissues"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
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HTC; CAP transociated
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P. Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
                                                                                                                                          Larninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                             Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                      HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaArgAlaSerGluLysPheAlaGlnThrValMetThrSerArgIleValGlyThrThr 352
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Rodentia;
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                                                                          Carninci, P.,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

AL Nature 420, 563-573 (2002)

CE 6 (bases 1 to 1161)

RB Adachi,J. Alzawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
Furuno,M., Hanagaki,T., Karai,J., Kojima,Y., Konno,H., Kouda,M.,
Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
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Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
Shibata,K., Tagami,M., Tagawa,A., Takhhashi,F., Tanaka,T.,
Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
Direct Submission
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                                                                                                                                    further details.

CDNA library was prepared and sequenced in Mouse Genome Exploration Research Group in Riken Encyclopedia Project of Genome Exploration Research Group in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand CDNA was primed with a primer 15' GAGAGAGAGAGATCTTTTTTTTTTTTTTTTTTVN 3'1, CDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through two rounds of normalization to Rot = 20.0 and subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 210-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, URLihttp://genome.gs.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
On Oct 4, 2001 this sequence version replaced gi:12860970. Please visit our web site (http://genome.gsc.riken.go.jp/)
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              nLeuGluGlnSerTyrMetProProAspSerSerSerProGluAsnLysSerLeuGluVa 160
                                                                                 lGlnGlnLysGlnMetProPheCysAspLysAspArgThrLeuMetThrProValGlnAs
                                                                                                                                                 LeuProAspAlaValProLysThrAlaAsnThrLeuProSerLysGluAla-IleThrVa
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ACTAGAACACAGCTGCGAGCCACCGGACTCCTC-AGCCCAGACAACAGAAGTGTAGAGTC
                                                                                                                            CTGCCGGATGCCGTTCCCCAAACCGTCAAAAGCCTGCCTAAAGAAGCGGGCAACAGT
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DDRYNQFHIRRFEALLQTGKSPTCELLFDWGTTNCTVGDLVDLLVQIELFAPATLLLF
DAVPQTVKSLPPKEAGNSGTNTRALSGNGQDIRNAYAKTRTQLRATGLLSPDNRSVES
SDTRFHSFSFHELKSITNNFDEQPASAGGNRMGEGGF"
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receptor-associated kinase 4 [Mu
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/clone_lib="RIKEN full-length
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57BL/6J"
/db_xref="FANTOM_DB:9330209D03"
/db_xref="MGI:19I1393"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAB32090.2"
/db_xref="GI:15919912"
/db_xref="MGI:1924812"
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|mol_type="mRNA"
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UI-R-FF0-cpj-c-20-0-UI 3', mRNA sequence.
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CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: DISTRIBUTION: Researchers may obtain clones
from Research Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 319 335 8250 Fax: 319 335 9565
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375 Newton Road , 4156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 6 (9), 791-806 (1996)
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sequence tags for these libraries are: CTAATGGACG CATTCTTGTA.
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/clone="UI-R-FF0-cpj-c-20-0-UI"
/tissue_type="Mixed tissues"
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 811)
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NIH-MGC http://mgc.nci.nih.gov/
                                                Homo sapiens
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                                                                                                          mRNA sequence
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Percent Similarity:
Best Local Similarity:
Query Match:
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ORIGIN
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  121
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM1645 row: p column: 17
High quality sequence start: 3
High quality sequence stop: 613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Institutes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: CLONETECH Laboratories, cDNA Library Arrayed by: The I.M.A.G.E. Consortium
GlnGlnLysGlnMetProPheCysAspLysAspArgThrLeuMetThrProValGlnAsn
                                                                                                                                                                                                       GlnThrGlyLysSerProThrSerGluLeuLeuPheAspTrpGlyThrThrAsnCysThr
                                         CTCCCAGATGCTGTTCCCCAAAACTGCTAATACACTACCTTCTAAAGAAGCTATAACAGTT
                                                               LeuProAspAlaValProLysThrAlaAsnThrLeuProSerLysGluAlaIleThrVal
                                                                                                                             GTTGGTGATCTTGTGGATCTTTTGATCCAAAATGAATTTTTCTGCTCCTGCGAGTCTTTTG
                                                                                                                                                ValGlyAspLeuValAspLeuLeuIleGlnAsnGluPhePheAlaProAlaSerLeuLeu
                                                                                                                                                                                                                                                                                             AMACCATCTGGTGATGATAGATACAATCAGTTTCACATAAGGAGATTTGAAGCATTACTT
                                                                                                                                                                                                                                                                                                                     LysProSerGlyAspAspArgTyrAsnGlnPheHisIleArgArgPheGluAlaLeuLeu
                                                                                                                                                                                                                                                                                                                                                                            AAGCTGTCAGATTTTATTGATCCTCAAGAAGGATGGAAGAAGTTAGCTGTAGCTATTAAA
                                                                                                                                                                                                                                                                                                                                                                                                       LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGAACAAACCCATAACACCATCAACATATGTGCGCCTCCAATGTTGGACTAATTAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_61"
/note="forgan: testis; Vector: pDNR-LIB (Clontech); Site_1:
/note="forgan: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAAAGGCCGACGACGG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."
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/db_xref="taxon:9606"
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935.50
81.10%
77.95%
39.21%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                           PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BU441365 769
603208981F1 CSEQRBN11 Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Biomolecular Sciences University of Manchester Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simon Hubbard
Department of Biomolecular Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGATGAACGACCCATTTCTGTCGGCGGTACTAACATGCGGAGGAGCGGAGGATTCGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuGluGlnSerTyrMetProProAspSerSerSerProGluAsnLysSerLeuGluVal 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---AspGlnGluIleLysValMetAlaLysCysGln 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerAspThrArgPheHisSerPheSerPheTyrGlu-LeuLysAsnValThrAsnAsn-P 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 769)
                                                                                                                                                                                                                                                                                                                                                                                                           Simon. Hubbard@umist.ac.uk.
/clone_lib="CSEQREN11"
/note="Vector: pBluescript II KS(+); Site_1: EcoRI;
Site_2: Not1; This normalized library was constructed from
1 million independent clones. cDNA synthesis was initiated
using an oligo(dT) primer, using methylated C in the first
strand synthesis reaction. Following this first strand
reaction, double-stranded cDNA was blunted, ligated to
                                                                                                                                                                                                   /sex="Male and female"
/tissue_type="muscle"
                                                                                                                                                                                                                                                                                        organism="Gallus gallus"

/mol_type="mRNA"

/strain="Layer and broiler"
                                                                                                                                                                                                                                                                                                                                                                               location/Qualifiers
                                                                                                                                                                                                                                                 clone="ChEST185a21"
                                                                                                                                                            dev_stage="adult"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:25930676
                                                                                                                                                                                                                                                                          xref="taxon:9031"
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    BF696981
LOCUS
DEFINITION
BF696981 719 bp mRNA linear EST 22-DEC-2000 602130160F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287014 5',
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NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
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	adapted from soares et al., rNAS (1994) 31: 9220-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was
BASE COUNT ORIGIN	230 a 146 c 180 g 213 t
Alignment Scorererent Simila Best Local Sir Query Match: DB:	3.29e-90 Length: 769 874.00 Matches: 166 11larity: 87.78 Conservative: 28 Similarity: 75.11 Mismatches: 26 1: 36.63 Indels: 1 13 Gaps: 0
US-10-001-2	254-16 (1-460) x BU441365 (1-769)
Ωу 2	34 IleLysValMetAlaLysCysGln-HisGluAsnLeuValGluLeuLeuGlyPheSerSe 2
Db	1 CTAGAAATTATGGCAAAGTGTAAACAATGAAAATCTGGTAGAATTGCTTGGTTTCTCAAG 60
Οу 2	
Db	61 TGATGGTGCTCAGCCCTGTTTGGTGTATGAATACATGCCCAATGGTTCGCTGCTTGACAG 120
Ωу 2	273 gLeuSerCysLeuAspGlyThrProProLeuSerTrpHisMetArgCysLysIleAlaGl 293
Db 1	21 ACTTGCTTGTCTGGATGGCACTCCACCTATTTCTTGGAAACACAAGGTGTGAAATTGCTCA 180
Qy 2	293 nGlyAlaAlaAsnGlyIleAsnPheLeuHisGluAsnHisHisIleHisArgAspIleLy 313
Db 1	81
Qy 3	313 sSerAlaAsnIleLeuLeuAspGluAlaPheThrAlaLysIleSerAspPheGlyLeuA1 333
Db . 2	41
0у з	333 aArgAlaSerGluLysPheAlaGlnThrValMetThrSerArgIleValGlyThrThrAl 353
Db 3	21
0у 3	353 aTyrMetAlaProGluAlaLeuArgGlyGluIleThrProLysSerAspIleTyrSerPh 373
Db 3	61
Qy 3	373 eGlyValValLeuLeuGluIleIleThrGlyLeuProAlaValAspGluHisArgGluPr 393
Db 4	21 TGGGGTAGTCTTACTAGAAGTAATAACAGGTCTGCCACCAGTAGACGAAAACCGGGAGC
Qy . 3	93
Db 4	81 A
Qy 4	413 rIleAspIysUsMetAsnAspAlaAspSerThrSerValGluAlaMetTyrSerValAl 433
Db 5	541 TGTTGACGTAAAGATGACTGGGATGCAACTTCAGTTCATAAAATGTATTCACTTGC 600
0у 4	433 aSerGlnCysLeuHisGluLysLysAsnLysArgProAspIleLysLysValGlnGlnLe 453
Db 6	01 TGATC
Qy 4	153 u 453
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RESULT 10	

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AUTHORS
TITLE
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VERSION
KEYWORDS
SOURCE
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BF696981
BF696981.1 GI
EST.
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Plate: LLCM1124 row: g column: 15
Pigh quality sequence stop: 632.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 719)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia, Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MCC clone distribution information can
                                                             GlnThrGlyLysSerProThrSerGluLeuLeu-PheAspTrpGlyThrThrAsnCysTh
                                                                                                                                       LysProSerGlyAspAspArgTyrAsnGlnPheHisIleArgArgPheGluAlaLeuLeu
                                                                                                                                                                                                                    LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLys 40
                                                                                                                                                                                                                                                                                                  MetAsnLysProIleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: CLONETECH Laboratories,
rValGlyAspLeuValAspLeuLeuIleGlnAsnGluPhe-PheAlaProAlaSerLeuL 100
                                                                                                                 AAACCATCTGGTGATGATAGATACAATCAGTTTCACATAAGGAGATTTGAAGCATTACTT
                                                                                                                                                                                                 AAGCTGTCAGATTTTATTGATCCTCAAGAAGATGGAAGAAGTTAGCTGTAGCTATTAAA
                                                                                                                                                                                                                                                                           ATGAACAAACCCATAACACCATCAACATATGTGCGCTGCCTCAATGTTGGACTAATTAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="primitive neuroectoderm"
/lab host="Drimitive neuroectoderm"
/lab host="Drimitive neuroectoderm"
/clone lib="NIH_MGC_56"
/clone lib="NIH_MGC_56"
/clone lib="NIH_MGC_56"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgcctggcc); Site_2: SfiI (ggccattatggcc);
SfiI (ggccgcctggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5;
and 3; adaptors were used in cloning as follows: 5
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCCGACAGCCGCCCAACTG-dT(30)BN-3'
(where B = A, C, Or G and N = A, C, G, Or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
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/clone="IMAGE:4287014"
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/mol_type="mRNA"
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856.00
91.43%
88.10%
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Conservative:
Mismatches:
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., E

Boardman, P.E., Sanz-Ezquerro, J., Wilson, S.A.

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A.

A Comprehensive Collection of Chicken cDNAs

A Comprehensive Collection of Chicken CDNAs

Courr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                              Tel: 01612008930
Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simon Hubbard
Department of Biomolecular Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                     Simon.Hubbard@umist.ac.uk
Location/Qualifiers
/clone_lib="CSEQCHN23"
/note="Organ: heads; Vector: pBluescript II KS(+); Site_1:
ECORI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with ECORI
, size-selected, and cloned into the NotI and ECORI
                                                                                                                                                                                /dev_stage="22"
/lab_host="DH10B"
                                                                                                                                                                                                                                     /strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
                                                                                                                                                                                                                      clone="ChEST902c19"
                                                                                                                                                                                                                                                                                                organism="Gallus gallus'
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CSEQCHN23 Gallus
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Percent Similarity:
Best Local Similarity:
Query Match:
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| SerValGluAlaMetTyrSerValAlaSerGlnCysLeuHisGluLysLysAsnLysArg
                                                                         AspGluGluLysThrIleGluAspTyrIleAspLysLysMetAsnAspAlaAspSerThr 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsnHisHisIleHisArgAspIleLysSerAlaAsnIleLeuLeuAspGluAlaPheThr 324
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                                                        GATGAGGAGGCGACTATAGAGGATTATGTTGACGTAAAGATGAGTGACTGGGATGCAACT
                                                                                                                                                                                                                                 ThrProLysSerAspIleTyrSerPheGlyValValLeuLeuGluIleIleThrGlyLeu
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                                                                                                                                                     ProAlaValAspGluHisArgGluProGlnLeuLeuAspIleLysGluGluIleGlu
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184 c 222 g 275 t 1 others
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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340084 BF
BG691069
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USDA, ARS, Belteville Agricultural Research
Bdlg. 200 Rm 2A, Belteville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases c
v0.980904.e. Vector identified
and -minmatch 12 options.
                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: ATTTAGGTGACACTATAG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Analysis of bovine mammary gland EST the Bos taurus gene index Mamm. Genome 13 (7), 373-379 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sonstegard, T., Capuco, A.V., White, J., V, Cho, J., Sultana, R., Shade, L., Wray, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos.

1 (bases 1 to 541)
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BACKWARD: GTTTTCCCAGTCACGACG
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AspArgTyrAsnGlnPheHisIleArgArgPheGluAlaLeuLeuGlnThrGlyLysSer
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                                                        ATTGATCCTCAAGAAGGATGGAAGAAGTTAGCAGTCGCTATTAAAAAAACCATCTGGTGAT
                                                                       IleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAsp
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                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="BARC 5BOV"
/clone_tib="BARC 5BOV"
/note=""vector: pcMV SPORT6; Site_1: NotI; Site_2: SalI;
/ibrary made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disea
states."

a 96 c 119 g 157 t
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Bos taurus
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                                                                                                                                                                              Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. .10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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1 (bases 1 to
    sequencing pipeline with 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y.,
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BB613167 RIKEN full-length enriched, 10
musculus cDNA clone 4732460I09 5', mRNA
BB613167
BB613167.1 GI:16453871
EST.
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Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihide Hayashizaki
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                  Hayashizaki,Y.
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                                                                                                                RIKEN integrated sequence analysis (RISA) system -- 384-format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGCCCCTCTGTGGCAAAGACAGGACATCTGTGATATCTGATGAGAATCCTGAACAAAAC 361
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81-45-503-9216
Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                      384 multicapillary sequencer. Genome Res.
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Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizaw,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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ValGlyAspLeuValAspLeuLeuIleGlnAsnGluPhePheAlaProAlaSerLeuLeu
                                                                        GlnThrGlyLysSerProThrSerGluLeuLeuPheAspTrpGlyThrThrAsnCysThr
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/lab_host="DH10B"
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410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                    Email: stephen.moore@ualberta.
Insert Length: 478 Std Error
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/note="Organ: Intestine/duodenum; Vector: Uni-2ZAPXR;
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                                                                                                                                                                                         /tissue_type="Smooth muscle"
/cell_type="Simple columnar epithelial"
/dev_stage="Young adult"
/lab_host="XL1-BlueMRF'strain"
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/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM902 row: p column: 23
High quality sequence stop: 564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 858) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collections to be seen that the collections of the seen that the collections are the seen that th
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Tissue Procurement: ATCC
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/tissue_type="glioblastoma"
/lab_host="DH10B (Tl phage-resistant)"
/clone_lib="NHH MCC 57"
/note="Organ: brain; Vector: pDNR-LIB (Clontech);
/sfil (ggccqtctggcc); Site_2: Sfil (ggccqttatggcc)
Double-stranded cDNA was prepared from cell line R
and 3' adaptors were used in cloning as follows: 5
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Location/Qualifiers
                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4066054"
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                                 ysGlnHisGluAsnLeuValGluLeuLeuGlyPheSerSerAspGlyAspAspLeuCysL 260
                                                                                                                                                                       TyrLysGlyTyrValAsnAsnThrThrValAlaValLysLysLeuAlaAlaMetValAsp 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuProAspAlaValProLysThrAlaAsnThrLeuProSerLysGluAlaIleThrVal 120
GGGTACATGGAAACTTAGCAGAAATACT-GGTTCTCCAGGTGAGGGGGATAAGCCCTGGG 661
                                                                                                                                                                                                                        ValGlyAspLeuValAspLeuLeuIleGlnAsnGluPhePheAlaProAlaSerLeuLeu 100
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                                                                                             | Ile-ThrThr-GluGluLeuLysGlnGlnPheAspGlnGluIleLysValMetAlaLysC 240
                                                                                                                                                TATAAAGGGTACGTAAATAACACAAT-GTGGGAGTGAAGACAGCTTGAGCAATGGTTGAC 545
                                                                                                                                                                                                                                                  AGTGATACACGTTTTCACAGTTTTTCATTTTATGAATTGAAGAATGTCACAAATAACTTG 427
                                                                                                                                                                                                                                                                                                                          SerAspThrArgPheHisSerPheSerPheTyrGluLeuLysAsnValThrAsnAsnPhe 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysProSerGlyAspAspArgTyrAsnGlnPheHisIleArgArgPheGluAlaLeuLeu 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLys 40
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                                                                          ATATACTACTGGAAGAACTGAAACAGCAGGTTGGATCAAGAATAAAG---TATGGGAAGT 602
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S 밁 S

260

euValTyrValTyrMetProAsnGlySerLeuLeuAspArgLeuSerCysLeuAspGlyT 280

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716_CTCCCCACTTTTTTGGGCATGGGAGGCCGAATTGGCCGGGGCGGCAAGGGGG 768	280 hrProProLeuSerTrpHisMetArgCysLysIleAlaGlnGlyAlaAlaAsnGly 298	:: 662 TAGGATATGTTACAGGCGCAAAGGGCATGGGAAACAAACTTTTGGTGTGGGGGG 715

Search completed: January 18, 2004, 06:06:50 Job time : 4501.9 secs

Score:

BEST AVAILABLE COPY

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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALICN=15 -MODE=LOCAL
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Ya Ishik,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki, Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 10633 09-JUL-2002;
HELIX RESEARCH INSTITUTE OS HOMO sapiens (human) PN JP 2002191363-A/10633
PD 09-JUL-2002
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Primer for synthesizing
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Novel death domain proteins
Patent: WO 0240680-A 25 23-MAY-2002;
BURNHAM INST (US)
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/translation="MMKPITPSTYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSG
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2 (bases 1 to 2213)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; CDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction,
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PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
                                                                                                                                                                                                                                        Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakawi, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AK027301 2213 bp mRNA linear Homo sapiens cDNA FLJ14395 fis, clone HEMBA1003250, to PROTEIN KINASE APKIA (EC 2.7.1.-).
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Primer for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
FT CDS (977). (1864).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                 Unpublished
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TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
SAITO,
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5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.)

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Scanlan, M.J., Stock
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/mol_type="mRNA"
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/note="cloning vector: pME1889
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SDTRFHSFSFYELKNVTNUNPDERPISTSVGGNNGEGGFFEVQNLEQGSYNNTTYAVKKLAN
VDITTEELKQQFDQEIKVMAKCQHENLVELLGFSSDGDDLCLVYVYMPNGSLLDRLSC
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/mol_type="genomic DNA"
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/db xref="taxon;9506"
/note="human IL-1 receptor-associated kinase 4 (IRAK-4)
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Roth,W. and Stenner-Liewen,F.
Novel death domain proteins
Patent: WO 0240680-A 15 23-MAY-2002;
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (Dases 1 to 1383)
Li,S., Strelow,A., Fontana,E.J
                                                           Homo
                                                                                                  AF445802.1
                                                                                                                          Homo sapiens interleukin-1 mRNA, complete cds.
                                                                                                                                                        AF445802
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="GI:21656176"
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/db_xref="GI:21656176"
/db_xref="GI:21656176"
/translation="makepitpertyvrcluvglirklsdeidpdegwkklavaikkpsg
DRYNQPHIRREALLQTGKS.PTSELLEDWGTTNCTVGDLVDLLIQNEFFAPASILLE
DAVPKTANTLESKEAITVQQKQMPFCDKDRTLMTPVQMLEQSYMPPDSSS.PENKSLEV
SDTRFHSFSTYELKNUTNNEDERPISVGGMKMGEGGFGVVYKGYVNTTVAVKKLAAM
VDITTEELKQQFDQEIKVMAKCQHENLYELLGFSSDGDDLCLVYVYMPSKILDRLSC
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                             Catarrhini;
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  and Wesche, H.
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Best Local Similarity:
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Suzuki,N., Suzuki,S., Duncan,G.S., Millar,D.G., Wada,T.,
Mirtsos,C., Takada,H., Wakeham,A., Itie,A., Li,S., Penninger,J.
Wesche,H., Ohashi,P.S., Mak,T.W. and Yeh,W.C.
Severe impairment of interleukin-1 and Toll-like receptor
signalling in mice lacking IRAK-4
Nature 416 (6882), 750-756 (2002)
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21957277
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/db_xref="G1:20219010"
/db_xref="G1:2021901
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/codon_start=1
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/mol_type="mRNA"
/db_xref="taxon:9606"
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7705840.

Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
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POLLLDIKEEIEDEEKTIEDVIDKKMNDADSTSVEAMYSVASQCLHEKKNKRPDIKKV
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/clone_lib="NIH_MGC_56"
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Roth,W. and Stenner-Liewen,F.
Novel death domain proteins
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ASEKFAQTVMTSRIYGTTAYMAPEALRGEITPKSDIYSFGVVLLEIITGLPAVDEHRE
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Scanlan, M.J., Gordan, J.D., Williamson, B., Stockert, E., Bander, N.H., Songeneel V., Gure, A.O., Jager, D., Jager, E., Knuth, A., Chen, Y.-T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (28-MAY-1999) Ludwig Institute, Sloan-Kettering Institute, 1275 York Ave, New York, NY 10021, USA
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Direct Submission
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Chen, Y.-T.
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                                                                                                                                                                                                     1 MetAsnLysProIleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg
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Shibahara, T., Tanaka, T.
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Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahar
Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
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                                                                                                    LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLys 40
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DDRYNQFHIRREALLQTGKSSPTSELLFDWGTTNCTVGDLVDLIQNEFFAPASILLP
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DAVPKTANTLPSKEAILYQGXQMPFCDKDRTIMTPVQNLBQSYMPPDSSSPENKSLEV
SDTRFHSFSFYELKNVTNNFDERPISVGGNKVGEGGFGVVYKGYVNNTTVAVKKLAAM
VDITTEELKQQFDQEIKVMAKQQHENLVELLGFSSDGDDLCLVYYYNENGSLLDRLSC
LDGTPPLSWHMRCKIAQGAANGINFLHENHHIRDIKSANILLDEAFTAKISDFGLAR
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/mol type="mRNA"
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/protein_id="BAA91232.1"
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/cell_type="signet-ring cell carcinoma"
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gene="TRAK4" frequency="0.01" replace="c"	/gene="IRAK4" /frequency="0.01" /freplace="c"	/25244. 25427,2659926661,2933629494,2961731033) /gene="IRAK4" /product="interleukin-1 receptor-associated kinase 4" 2315	.11209,1415714302,15117 6966,2056720681,21130	replace n 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	/replace="y" (" )	/replace="a" 1265	type=dispersed uencv="0.02"	/replace="c" 708941 /ret familv="12"	42 frequency="0.02"	/rpt_type=dispersed	replace="a" replace="a"	33 33 33	frequency="0.02"	rpt_tamily="Alu" rpt_type=dispersed	rpt_type=dispersed	.88 family="12"	organism="Homo sabiens"  mol_type="genomic DNA"  db xref="taxon:9606"	ion/Qualifiers	for Genomic Applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).	NHIBI HISSS	iversity of	J. Armel, T.Z., Carrington, D.P., Ozuna, M., Kuldanek, S.A.,	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Sutheria; Primates; Catarrhini; Hominidae; Homo.   to 32032	(human)	:26000792	AY186092 33033 bp DNA linear PRI 02-DEC-2002 Homo sapiens interleukin-1 receptor-associated kinase 4 (IRAK4) gene, complete cds.		AAACCATCTGGTGATGATAGATACAATCAGTTTCACATAAGG 191
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Submitted (09-AUG-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 118572) Worley,K.C.
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Homo sapiens 12 BAC RP11-210N13 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
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1 (bases 1 to 118572)
                                                                                                                                                    Worley, K.C.
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                                                                                                                                                                                           QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base such that 1 per 10,000 bases are reports of lowest quality because of bases are reports of lowest quality are listed below. Description of the metrics can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (24-SEP-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
On Jun 29, 2002 this sequence version replaced gi:21535906.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                               SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
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Submitted (29-002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA (lases 1 to 118572)
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Baylor Plaza, Houston,
4 (bases 1 to 118572)
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ted (04-JUN-2002) Human Genome Sequencing
ecular and Human Genetics, Baylor College
Plaza, Houston, TX 77030, USA
                                                                                                              Location/Qualifiers
           /mol_type="genomic_DN.
/db_xref="taxon:9606"
/chromosome="12"
                                                                  organism="Homo sapiens"
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/rpt_family="L2"
7574. .8066
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17329. .17356
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complement(15692..15972)
/rpt_family="AluSc"
16265..16352
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14363.
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complement(4612. .477
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16632. .17007
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Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Durkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., McKernan, K.,
McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., McKernan, K.,
Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K.,
Pierre, N., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman n
Direct Subminder, A., and Zody, M.
Lifect Submitted (19-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Genome Research, 320 Charles Street, Cambridge, MA 02141, USA CE 3 (bases 1 to 165868)

Example 1 to 165868)

Example 1 to 165869

Example 2 to 165869

Example 3 theon, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bestien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McGarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Rell, D., Ollvar, T. M., Shojanovic, N., Shojanovic, N., Shojanovic, N., Shojanovic, N., Shojanovic, N., Shojanovic, N., Travers, M., Trigilio, J., Vaessiliev, H., Viel, R., Vo, A., Wilson, B., Wi, X., Wyman, D., Ye, W.J., Timmer, A. and Zody, M.
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 19, clone RP11-210N13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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misc_feature
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All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 156294 bases at least Q40

Consensus quality: 160271 bases at least Q30

Consensus quality: 162203 bases at least Q20

Insert size: 175000; agarose-fp

Quality coverage: 4.9 in Q20 bases; agarose-fp

Quality coverage: 5.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: L5945
Center clone name: 210_N_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
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107725
123978
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/clone lib="RPCI-11 Human Male
1. .1982
/note="assembly_fragment"
                                                                      map="19"
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                                                                                                                       type="genomic
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Best Local Similarity:
Query Match:
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                                                                                                                                                                            AX321132 501 bp
Sequence 149 from Patent W00177168.
AX321132
AX321132.1 GI:17904576
Patent: WO 0177168-A 149 18-OCT-2001;
CORIXA CORPORATION (US)
Location/Qualifiers
                                                        Lodes, M.J., Wang, T., Mohamath, R. and Indirias, C.Y. Compositions and methods for the therapy and diagnosis of lung
                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Homo sapiens
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망	ş	Db	Ş	Дb	Ş	US-10-	DB:	Query Match:	Best L	Percen	Pred. No.:	Alignm	ORIGIN	BASE COUNT		ω.
141 AAACCATCTGGTGAT	41 LysProSerGlyAsp	81 AAGCTGTCAGATTTT	21 LysLeuSerAspPhe	21 ATGAACAAACCCATA	1 MetAsnLysProlleThrProSerThrT	US-10-001-254-26 (1-59) x AX321132 (1-501)	თ		ty:	Percent Similarity: 98.18%	No.: 2.97e-29	Scores:	1	/db_3	/organis /mol typ	source 1501
AAACCATCTGGTGATGATAGATACAATCAAGTTTCACATAAGG	LysProSerGlyAspAspArgTyrAsnGln-PheHisIl	AAGCTGTCAGATTTTATTGATCCTCAAGAAGGATGGAAGAAGTTAGCTGTAGCTATTAAA	LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuA	ATGAACAAACCCATAACACCATCAACATATGTGCGCTCCTCAATGTTTGGACTAATTAGG	yrVal	321132 (1-501)	Gaps:				e-29 Length:		ŭ	db_xref="taxon:9606"	organism="Homo sapiens" mol type="genomic DNA"	
  AGG 183	eArg 54	AAGTTAGCTGTAGCTATTAAA 140	ysLeuAlaValAlaIleLys 40	TCAATGTTGGACTAATTAGG 80	ArgCysLeuAsnValGlyLeuIleArg 20		0	<b>+</b>	0		501 54			2 others		

Search completed: January 18, 2004, 04:27:07 Job time : 1025.41 secs

BEST AVAILABLE COPY

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-MODELI-frame+ D2n.model -DEV=Xlh
-Q=/Ggn2 1/USPTO_spool/US1001254/runat 16012004 152424 19723/app_query.fasta_1.1109
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## DNA moding sea 26

ALIGNMENTS

EST 13-NOV-1996

RESULT 1 AA114228 LOCUS DEFINITION

AA114228

284 bp mRNA linear EST 13-NOV-19
zn75905.rl Stratagene NT2 neuronal precursor 937230 Homo sapiens
cDNA clone IMAGE:564056 5', mRNA sequence.
AA114228

AA114228.1 GI:1668121

ACCESSION VERSION

KEYWORDS SOURCE ORGANISM Homo sapiens Homo sapiens (human)

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 284)

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800 Fax: 314 286 1810
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                          mRNA sequence.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                  Homo sapiens
                                              Homo sapiens (human)
                                                                                                 BF238344
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                                                                                                                                                                                                            AAACCATCTGGTGATGATAGATACAATCAGTTTCACATAAGATGCTGTTCCCAAAAC 237
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                540 bp DKFZp686K18112 rl 686 (synonym: DKFZp686K18112 5', mRNA sequence
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM1032 row: i column: 03
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Tissue Procurement: ATCC
                                                                                                                  Homo sapiens (human)
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/lab host="phi0B (T1 phage-resistant)"
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/clone="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
/clone="Organ: bone marrow; Vector: pDNR-
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 719)

NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                  broy6981 719 bp mRNA line 60213016051 NIH_MGC_56 Homo sapiens cDNA clone
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                                                                                                                                   BF696981.1 GI:11982389
                                                                                                                                                        BF69698
                                                                                                                                                                        mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone (DKFZp686K18112) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: poustka@mpimg-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Max-Planck-Institute for Molecular Genetics Innestrasse 73, 14195 Berlin, Germany Tel: +49-30-84131623
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Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).

EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann
                                                                           Homo sapiens
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/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"
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/dev_stage="adult"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 811)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                  602642772F1 NIH_MGC_61 Homo
                                                                                                                                                         Homo sapiens
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Tissue Procurement: ATCC
                                                                                                                                                                                          Homo sapiens (human)
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Plate: LLCM1124 row: g column: 15
High quality sequence stop: 632.
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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/clone_lib="NIH_MGC_66"
/clone_lib="NIH_MGC_66"
/clone_lib="NIH_MGC_66"
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/db_xref="taxon:9606"
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                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 859)
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602342026F1 NIH_MGC_89 Homo sapiens
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Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                       BG164491
BG164491.1 GI:12671194
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                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                          mRNA sequence.
                                                                                                                                                            Homo sapiens (human)
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/lab host="DH10B (TI phage-resistant)"
/clome_lib="NIH_MGC_61"
/clome_lib="NIH_MGC_61"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: testis; Vector: pDNR-L
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity:
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TCBAP1E11457 Pediatric pre-B cell acut
Baylor-HGSC project=TCBA Homo sapiens
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Contact: Robert Strausberg, I
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 313)

Wei,Y., Tsang,Y T.M., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr., Gunaratne,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F. Gediatric Leukemia cDNA Sequencing Project (2001)
                                                            Unpublished
                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 634.
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Plate: LLAM10240 row: d column: 08
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/tissue type="hypernephroma, cell line"
/lab_host="PH108 (phage-resistant)"
/clone_lib="NIH MGC_89"
/clone_lib="NIH MGC_89"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."
a 168 c 190 g 235 t
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/db_xref="taxon:9606"
/clone="IMAGE:4452055"
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RESULT 8
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Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@txccc
                                                                                                                                              265 bp
76774 MARC 2PIG Sus scrofa cDNA
AW436511
AW436511.1 GI:6971817
EST.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 265)
Fahrenkrug,S.C.; Smith,T.P.L., Freking,B.A., Cho,J. Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,J. and Keele,J.W.
                                                                                                            Sus scrofa (pig)
Sus scrofa
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primer: M13 primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leukemia Baylor-HGSC project=TCBA"

/note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer [5'GRAGGAGTCGAGCGCGCAGGAGGAGGA(T) VN
3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand
was primed with a BamHI-dC primer
[5'AGAGAGCTCGAGTCGCGCGCGCAATAATAATAAT(C) 3'].
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamHI and SalI sites of
lambda pSB vector. Library was constructed by Wei Yu at RIKEN
of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M,
Schneider C, Hayashizaki Y, High efficiency selection of
full-length cDNA by improved biotinylated cap trapper.,
DNA Res 4: 1, 61-6, Feb 28, 1997)"
10 thers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="pre-B cell"
/dev_stage="pediatric 2
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Matches:
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                 , Cho,J., Wh: Sultana,R.,
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                                                                         Euteleostomi;
Sus.
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           White,J.,
R., Quackenbush
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                                 Quackenbush, J.
Analysis of bovine mammary
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
                                                                                                                               Bos taurus
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BE482619
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                                                                                                                                             Bos taurus (cow)
                                                                                                                                                                            BE482619.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
Single pass sequencing. Bases call
v0.980904.e. Vector identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USDA, ARS, US Meat Animal PO Box 166, Clay Center, N Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mamm.
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Bos taurus gene index
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/lab_host="DH108"
/lab_host="DH108"
/clone_lib="MARC_2PIG"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
/inote="Vector: pcMV SPORT6; Site_1: NotI; Site_2: SalI;
/ibrary made from pooled tissue from testis, ovary,
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
s 53 c 58 g 64 t
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98.15%
98.15%
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xref="+~"
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Fax: 301 504 8414
Email: talana
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayateu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konda, M., Matsuyama, T., Y., Ito, M., Nishi, K., Nomura, Y., Komasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 453)
                                                                                                                                                                                BB860349.1 GI:17101803
EST.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                BB860349 MTKEN full-length enriched, pooled cDNA clone G430013H14 5', mRNA sequence.
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Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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BACKWARD: GTTTTCCCAGTCACGACG
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/lab host="PHIOB"
/lab host="PHIOB"
/clone lib="BARC 5BOV"
/clone lib="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
/ibrary made from pooled mRNA isolated from mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
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URL:http://genome.gsc.riken.go.jp,

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Tanaka,T., Matsuura

,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and

Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,
, Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      further details
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/clone lib=RIKEN full-length enriched, pooled cell lines,
/clone lib=RIKEN full-length enriched, pooled cell lines,
/clone lib=RIKEN full-length enriched,
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/clone lib=RIKEN full-length enriched,
/cell line=RCB-035 WEH1 3),
/cell line=RCB-0464 Meth-A), (cell line=RCB-035 WEH7),
/cell line=RCB-0559 K.1 . Fl), (cell line=RCB-0545 OHTA),
/cell type=Bullipotent ells, cell line=CRL-2070 WEHI 231
/cell type=Nullipotent stem cell, cell line=CRL-2070 WEHI 231
/cell type=bladder, cell line=RCB-0544 MBT-2),
/cell sue type=bone marrow, cell type=stroma cell,
cell line=CRL-2028 SR-4987), (tissue type=colon,
cell line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,
cell line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,
cell type=B cells, cell line=CRL-1669 BCL1 Clone 13.20-3B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ), (strain=C3H, tissue_type=brain, cell_line=CRL-1443
BC3H1)"
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/db_xref="taxon:10090"
/clone="G430013H14"
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271.00
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83.90%
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 Cassell Drive, Suite 4000, Ba Email: cdna@lgsun.grc.nia.nih.gov Plate: C0272 row: B column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
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Other_ESTs: C0272B01-3
Contact: Dawood B. Dud
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: M13 Reverse
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1 (bases 1 to 503)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 503
/tissue_type="whole embryo including extraembryonic
tissues at 7_5-days postcoitum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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(Long)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
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/strain="C57BL/6J"
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                                                                                                                                     Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinagawa, A., Shinaki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetAsnLysProIleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Su, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                        1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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146 c 138 g
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Rodentia;
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RESULT 13
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                      524 bp
um23h11.yl Sugano mouse embryo n
INAGE:2225445 5', mRNA sequence
AW106160
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                                                                                                                                                                                                                    Mus musculus (house mouse)
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                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clone pooled cell lines; (cell line=RCH-1751 WEHI 164),
(cell line=RCH-2116 JC), (cell line=RCB-0035 WEHI-3),
(cell line=RCB-0464 Meth-A), (cell line=RCB-0545 OHTA),
(cell line=RCB-0559 K-1 F1), (cell line=RCB-1283 B16
(cell line=RCB-0559 K-1 F1), (cell line=RCB-1283 B16
(cell type=Leydig cells, cell line=CRL-1702 WEHI 231
), (cell type=Nullipotent stem cell, cell line=RCH-2070 NE),
(tissue type=bone marrow, cell line=RCB-0544 MBT-2),
(tissue type=bone marrow, cell type=stroma cell,
cell line=RCB-0549 Cle-H3), (tissue type=colon,
cell line=RCB-0549 Cle-H3), (tissue type=boland,
cell line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,
cell type=B cells, cell line=CRL-1669 BCL1 Clone 13.20-3B3
cell type=B cells, cell line=CRL-1669 BCL1 Clone 13.20-3B3
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/mol_type="mRNA"
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                                     27-MAY-2003
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RZPD Mus musculus cDNA clone IMAGp998L225504 = IMAGE:2225445 5' EST.
                                                                                                                                       BX522921;
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Other_ESTs: um23h11.x1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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/clone_lib="Sugano mouse embryo mewa"
/note="Vector: pME185.FL3; Site_l: DraIII (CACTGTGTG);
/note="Vector: pME185.FL3; Site_l: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); lst strand cDNA was primed with an oligo (dr) primer [ATGTGGCCTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME185.FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' med primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCACCTCAACACAA."
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/lab_host="DH10B"
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'clone="IMAGE:2225445"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heubnerweg 6, D-14059 Berlin,
Tel: +49 30 32639 101
Fax: +49 30 32639 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=981
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Mouse UnigeneSet - RZPD2 (RZPDLIB No.981)
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                    /mote='lst strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME188-FL3 vector [5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTGAGCACA. REFERENCES: Suzuki, Y., Yoshitom and characterization of a full length-enriched and a 5' end enriched cDNA library. Gene 200, 149-156, 1997. Sasaki, Z., Suzuki, Y., Watanabe, M., Imai, J., Shibui, A., Yoshida, K., Hata. H., Yamaguchi, R., Tateyama, S., and Sugano, S. Construction of mouse full length-enriched cDNA libraries by oligo-capping. DNA Research. submitted."
                                                                                                                                                                                                          BP;
                                                                                                                                                                                                                                                                                               by oligo-capping. DNA Research, /organism="Mus musculus"
                                                                                                                                                                                                                                                  /clone="IMAGp998L225504"
/clone_lib="Sugano mouse embryo
/dev_stage="embryo, 14 dpc"
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yong Qian
Laboratory of Genetics
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
33 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
Plate: H4014 row: C column: 09
Plate: H4014 row: C column: 09
Seg primer: -21M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 598)
1 (bases 1 to 598)
VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., C., P.R., Stagg, C.A., Bassey, U., Aiba, K., Hamatani Luo, A.G., Kelso, J., Hide, W. and Ko, M.S.H. Assembly, verification, and initial annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA clone set
Genome Res. 12 (12), 1999-2003 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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MetAsnLysProIleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg
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/lab_host="DH10B"
/clone lib="NIA Mouse 7.4K cDNA Clone Set"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
/note="Vector: pSPORT1; Site_1: SalI; SalI; Site_2: NotI; This
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
/note="Vector: pSPORT1; Site_1: SalI; Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="niaEST:H4014C09-5"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex="mlxed"
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Rodentia; Sciurognathi;
                                                                                     (1-598)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone
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152

211

21 LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLys 40	Search Job ti	ф	ş	Db	Ş
	Search completed: January 18, 2004, 06:06:52 Job time : 578.135 secs	272 AAGCCGTCCGGCGACGACAGATACAATCAGTTCCATATAAGG 313	41 LysProSerGlyAspAspArgTyrAsnGlnPheHisIleArg 54	212 AAGCTGTCGGATTTTATTGATCCTCAAGAAGGGTGGAAGAAATTAGCAGTAGCTATCAAA 271	21 LysLeuSerAspPhelleAspProGlnGlvGlyTrpLysLysLeuAlaValAlaIleLys 40

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-Q=/Ggn2_1/USPTO_SDOO1/USLICONIST.
-Q=/Ggn2_1/USPTO_SDOO1/USLICONIST.
-Q=/Ggn2_1/USPTO_SDOO1/USLICONIST.
-DB=N Geneseq_19Jun03 -OPMT=fastap -SUFFTX=r1g -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN-0 -ALIGN=15
-MODE=LOCAL -OUTFMT-pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10001254 @CGN 1 1 0 @runat 16012004 152423 19704 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Command line parameters: -MODEL=frame+_p2n.model
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Maximum DB
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Ygapop 10.0
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

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Human IRAK4 short gene.		22-OCT-2002		AAD40084;		AAD40084 standard; DNA; 211 BP.	AAD40084	ILT 1 ·	
(4 short g		)2 (first entry)				standard;			
ene.		enti				DNA;			
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						BP.			

ALIGNMENTS

	Human; death domain; DD; death effector domain; DBD; Chlamydia infection;
_	NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;
_	inflammation; allergy; autoimmunity; allograft rejection; cell division;
	immune-based pathology; fibrosis; arthritis; graft versus host disease;
	immunosuppressive; gene therapy; antisense therapy; gene; ds.
	Homo sapiens.

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                                                                                           US-10-001-254-26
                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain CD or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or NB-NBC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or NB-NBC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation allergy, sepsis, autoimmunity, allograft rejection and other disease
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29-JUN-2001; 2001US-301889P.
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                   MetAsnLysProIleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg
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iewen F;
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                      polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in discretize forencies cape marking identification of mutations.
                                                                                                          diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity -
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23-AUG-2000; 2000US-0649167.
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                                                                        ftp.wipo.int/pub/published_pct_sequences.
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   144 A; 83 C;
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Alignment Scores: Pred. No.:

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RESULT 3
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Best Local Similarity:
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             The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5 end sequence and an oligonucleotide comprises a 3 end sequence complementary to a polynucleotide which comprises a 5 end sequence and sequence which comprises a 5 end sequence complementary to a polynucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in the specification. The primer sets can be used in antisense therapy and the specification.
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Ishii :
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                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID 10742; 2537pp +
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02-MAY-2000;
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27-AUG-1999;
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99JP-0300253.
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ı A, Nagai K
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Best Local Similarity:
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Stockert
                                               WPI; 2000-303774/26.
P-PSDB; AAY92347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the protein and acid sequences.
                                                                                                                              05-OCT-1998;
05-OCT-1998;
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                                                                                                                                                            04-OCT-1999;
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                                                                                                                                                                                                                                                                                   cytostatic;
                                                                                                                                                                                                                                                                                            renal cancer;
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E, Chen
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                                                                           Pfreundschuh Knuth A;
                                                                                                                                                                                                                                                                                            precursor; diagnosis;
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Preventing, diagnosing abnormal expression of

and/or treating human cancer ass

associated antigens disorders associated

Claim 57; Page 85; 121pp; English

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis; behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor; sarcoidosis; transgenic animal; ss.
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      13-JAN-2000; 2000US-0176395
                                                                  12-JAN-2001; 2001WO-US01171.
                                                                                                                                       19-JUL-2001.
                                                                                                                                                                                                          WO200151641-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 cDNA.
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                                                                                                                                                                                                                                                                        /product= "Human IRAK-4"
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CC inhibitors are useful for treating inflammatory diseases such as CC pulmonary diseases and diseases of the airway (e.g., adult respiratory CC disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD), CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough CC or allergic rhinitis), transplant rejection, autoimmune diseases (e.g., CC rheumatoid arthritis, systemic lugus erythematosus, multiple sclerosis or diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma), CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases (c.g., stroke and atherosclerosis), diseases (c.g., fihe central mervous system (e.g., neurodegenerative disease), CD14 mediated sepsis, non-CD14 mediated sepsis, osteoparthritis, osteoporosis, CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and CC dermatitie), inflammatory bowel disease (e.g., Crohn's disease and CC dermatitis), Behcet's syndrome, ankylosing spondylitis, gout, CC sarcoidosis and ophthalmic diseases and conditions. The inhibitors of CC resulting from the activation of an interleukin-1 receptor (IL-IR)/Toll CC receptor in a cell. They also inhibit the activation of a transcription CC factor that activates NFkappaB in the cell. IRAK-4 is used to create a CC for IRAK-4 in vivo, to generate models for the study of inflammatory CC disorders and conditions and for the development of potential treatments for IRAK-4 in vivo, to generate models for the study of inflammatory treatments and conditions. IRAK-4 sequences of the study of inflammatory diseases and conditions. IRAK-4 sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)-kappaB activation. The IRAK-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating asthma, allergic rhinitis, multiple sclerosis and skin cancer -
Sequence 1383 BP; 463 A; 244 C; 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a cDNA encoding human interleukin (IL)-1 receptor associated kinase (IRAK)-4. IRAK associate with activated IL-1, IL-18
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P-PSDB; AAE05398.
                                                           are also used in gene therapy and in antisense therapy.
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     G; 393
        T; 0 other;
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Percent Similarity:
Best Local Similarity:
Query Match:
                                      No.:
2.43e-34
290.00
100.00%
100.00%
89.78%
22
                              Length:
Matches:
               Conservative: Mismatches:
         Indels:
1383
54
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US-10-001-254-26 (1-59) x AAD10197 (1-1383)

Gaps:

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RESULT 6
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AC AAD4
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                                                                                                            LysProSerGlyAspAspArgTyrAsnGlnPheHisIleArg
                                                                                                                                                                 LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLys
                                                                                                                                                                                                          ATGAACAAACCCATAACACCATCAACATATGTGCGCTGCCTCAATGTTGGACTAATTAGG
                                                                                                                                                                                                                         MetAsnLysProIleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg
                                                                                              AAACCATCTGGTGATGATAGATACAATCAGTTTCACATAAGG
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AAD40079

AAD40079 standard; DNA; 1383

ВP

22-OCT-2002

(first entry)

IRAK4 gene

120

60

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Alignment Scores: Pred. No.:
                                                                                             CC is useful for identifying a binding agent, preferably a protein or a drug CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or CC MIDD (NGFR-interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent and CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (TV) or CC chemical crosslinking, nuclear magnetic resonance (NMR), mass CC spectroscopy (MS) and FPA. The invention is useful for modulating the clevel of a cell process such as cell proliferation, cell adhesion, cell elvel of a cell process such as cell proliferation and B cell communoglobulin class switching, in particular apoptosis within a cell communoglobulin class switching, in particular apoptosis within a cell communoglobulin class switching, in particular apoptosis within a cell communidation, c. pneumoniae, and C. psittaci or a nucleic acid encoding the CTDD DD protein is useful for detecting a Chlamydia infection. The class switching the activity of oncogenic proteins, cc for treating bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for classovery of drugs that suppress infection, and other diseases. The protein and contact contact and conta
                                                                                                                                                     sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense
                                                                                          Sequence
                                                                                                                                         therapy and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB-ARC domain. The inve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 19; Page 180-182; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other disease
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Stenner-liewen
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29-JUN-2001;
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DB; AAE24859.
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2001US-301889P.
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                                                                                                                                         therapy. The present sequence is human
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                                                                                                                                    IRAK4 gene
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RESULT 7
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Best Local Similarity:
Query Match:
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                                                                         polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in distance in the content of the content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and
                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 12609; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                      Human; death domain; DD; death effector domain; DED; Chlamydia infection; NB-ARC domain; apoptosis; oncogenic protein, bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy; gene; ds.
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New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases
                                                                                            Reed JC, Godzik A, Stenner-liewen F;
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29-JUN-2001; 2001US-301889P
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DB; AAE24865.
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/*tag= ?
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                /product= "Human IRAK4"
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290.00
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89.78%
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Mismatches:
Indels:
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                                  The invention relates to an isolated polypeptide comprising a death CCC domain (DED) or NB-ARC domain. The invention consists and isolated polypeptide comprising a death CCC domain for identifying a binding agent, preferably a protein or a drug CCC that binds a DD, DED or NB-ARC domain. By contacting a DD, DED or NB-ARC CCC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or NIDD (NGFR-interacting Death Domain), with a candidate binding agent, DED4 or NIDD (NGFR-interacting Death Domain), with a candidate binding agent and CC detecting the association of the domain and the candidate binding agent compared two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or CC chemical crosslinking, nuclear magnetic resonance (NMR), mass cc level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and B cell compared to facely specifically reactive with CTDD DD of C. trachomatis, C. CC compared to microbial infection and B cell convention is useful for modularing the activity of oncogenic proteins, cell convention is useful for detecting a Chlamydia infection. The CC convention is useful for modularing the activity of nocogenic proteins, cell convention. The protein and antibody specific for it are useful for creating bacterial infections by modularing the activity of bacterial convention. The protein and antibody specific for it are useful for cell division, inflammatory diseases such as sepsis. The protein cell convention, allergy, and gene therapy. The present sequence is human IRAK4 gene.

CC arthritis, graft versus host disease. The invention is used in antisense convention is used in antisense.
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B₽;
912 A; 547
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  586 G;
     772
     T; 0
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Percent Similarity: Best Local Similarity: US-10-001-254-26 (1-59) x AAD40085 (1-2817) Query Match: Alignment Scores: 6.32e-34 290.00 100.00% 100.00% 89.78% Length:
Matches:
Conservative: Gaps: Mismatches: Indels: 2817 54 0 0

밁 5 밁 S Ś 110 41 21 50 Н MetAsnLysProIleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLys 40 LysProSerGlyAspAspArgTyrAsnGlnPheHisIleArg 54 109

RESULT 9

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170

211

AAS61608 standard; CDNA;

AAS61608;

29-JAN-2002 (first entry)

Lung small cell carcinoma antigen, cDNA #149

Human; cytostatic; antitumour; lung small cell cancer antigen;

tumour; lung cancer;

AAS61608

ID AAS6
XX
AC AAS6
AC AAS6
AX 29-J
DE Lung
XX
XX
XX
Lung
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XX
CHUM
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CHUM WO200177168-A2

18-OCT-2001

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RESULT 10
AAD10198
ID AAD10
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AC AAD10
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                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotide hybridised to (III) in the sample and comparing the amount of polynucleotide to a predetermined cut-off value and thereby determining cancer in a patient. (I), (II) or antigen-presenting cells expressing (II) is useful for stimulating and/or expanding T cells specific for a tumour protein. The method comprises contacting T cells with one of the components under conditions to permit the stimulation and/or expansion of the cells. A composition comprising (I) is useful for stimulating an immune response in a patient and for inhibiting the development of a cancer especially lung cancer in a patient. An isolated T cell population is useful for removing tumour cells from the biological sample and for inhibiting the development of cancer in a patient. AASG180-AASG1874 represent over human lung small cell cancer in the cancer and for inhibiting the development of cancer in a patient.
                 24-SEP-2001
                                              AAD10198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel isolated lung small cell cancer antigen polymucleotides (I) and polypeptides (II) used in a method of detecting cancer in a patient. The method is optionally performed by utilising oligonucleotides (III), where the biological sample from the patient is contacted with (III), detecting the amount of
                                                                          AAD10198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer antigen
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21-JUN-2000;
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2000US-213361P.
2000US-229763P.
2000US-230629P.
2000US-232565P.
2000US-257037P.
2001US-260796P.
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               (first entry)
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Mouse interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4 cDNA.
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Mouse; interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic; II; antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD, chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoparthritis; rash; osteoprosis; psoriasis; dermatitis; inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis; Behcet's syndrome; ankylosing spondylitis; II-1 receptor/Toll receptor; sarcoidosis; transgenic animal; ss.

Mus sp

Key Location/Qualifiers
CDS 1..1542
/*tag= a
/product= "Mouse IRAK-4"

WO200151641-A1

19-JUL-2001.

12-JAN-2001; 2001WO-US01171

13-JAN-2000; 2000US-0176395

(TULA-) TULARIK INC.

Wesche H, Li S;

WPI; 2001-451860/48

Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating gout, asthma, allergic rhinitis, multiple sclerosis and skin cancer -

Claim 26; Fig 4; 89pp; English.

CC The present sequence is a cDNA encoding mouse interleukin (IL)-1 receptor CC associated kinase (IRAK)-4. IRAK associate with activated IL-1, IL-18 CC and other receptors and act to transduce signals originating from the CC effects such as nuclear factor (NP)-kappaB activation. The IRAK-4 CC inhibitors are useful for treating inflammatory diseases such as CC pulmonary diseases and diseases of the airway (e.g., adult respiratory CC disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD), CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough CC or allergic rhinitis), transplant rejection, autoimmune diseases (e.g., CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis CC or diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma), CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases CC of the central nervous system (e.g., neurodegenerative disease), CD14 cardiovascular diseases of the skin (e.g., rash, contact dermatitis, atopic CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and CC dermatiting from the activation of an interleukin-1 receptor (IL-IR)/Toll receptor in a cell. They also inhibit the activation of a transcription CC resulting from the activation of an interleukin-1 receptor (IL-IR)/Toll receptor in a cell. They also inhibit the activation of a transcription of activation and for the study of inflammatory disease and CC disorders and conditions and for the development of potential treatments CC disorders and conditions and for the development of potential treatments CC are also used in gene therapy and in antisense therapy.

Sequence 1542 BP; 421 A; 392 C; 423 G; 306 T; 0 other;

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RESULT 11
AAD40074
ID AAD40
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                                                       New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation allergy, sepsis, autoimmunity, allograft rejection and other diseas
                    Claim 18; Page 173-174;
                                                                                                      WPI; 2002-500222/53
P-PSDB; AAE24854.
                                                                                                                                         Reed JC, Godzik A, Stenner-liewen F;
                                                                                                                                                                                                   17-NOV-2000; 2000US-0715893
29-JUN-2001; 2001US-301889P
                                                                                                                                                                                                                                                                                                                                                                                                                            Human; death domain; DD; death effector domain; DBD; Chlamydia infection; NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD40074 standard;
                                                                                                                                                                                                                                      15-NOV-2001; 2001WO-US44844.
                                                                                                                                                                                                                                                                                       WO200240680-A2
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (death domain) cDNA.
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/note= "No start and stop of partial"
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                    209pp; English
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                                                       inflammation, other diseases
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                                                                                                                                                                               US-10-001-254-26 (1-59) x AAD40074 (1-294)
                                                                                                                                                                                                                                                                                                                       Score:
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                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 294
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13
                            29 GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr
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                                                                                        1 ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
CAAGAAGGATGGAAGAAGTTAGCTGTAGCTATTAAAAAAACCATCTGG
                                                                                                                   ThrTyrValArgCysLeuAsnValGlyLeuIleArgLysLeuSerAspPheIleAspPro
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247.00
100.00%
100.00%
76.47%
24
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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0 0
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## S 묽 121 49 AsnGlnPheHisIleArg 54 138

AAA16683 ID AAA:

AAA16683 standard; cDNA; 5170

AAA16683;

16-JUN-2000 (first entry)

Human secreted protein clone nf56_3 nucleotide sequence SEQ ID NO:131.

infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus; connective tissue disease; multiple sclerosis; erythematosis; rhoumatoid arthritis; autoimmune pulmonary inflammation; asthma; Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis; insulin dependent diabets mellitus; graft-versus-host-disease; autoimmune inflammatory eye disease; allergy; ss. antibacterial; antifungal; cytostatic; antiinflammatory; dermatological; antidiabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide; antithyroid; immune deficiency; severe combined immunedeficiency; SCID; Human; secreted protein; immunestimulant; immunesuppressant; virucide;

invention relates to an isolated polypeptide comprising a death

WO200009552-A1

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CC AAY94980 to AAX94980, isolated from human adult brain, adult thyroid, CC adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney, CC adult placenta, adult testis, whole embryo, adult cartilage, kidney, CC adult placenta, adult thymus, foetal placenta, adult uterus, adult turous, adult thymus, foetal placenta, adult turous, adult thomour, CC and adult bladder, cDNA libraries. The polynucleotides and proteins are predicted to have biological activities which would make them suitable CC for treating, preventing or ameliorating medical conditions in humans are considered to have biological activities which would make them suitable CC and adult bladder, cDNA libraries. The polynucleotides can be used as markers for tissues in which the protein is preferentially expressed, as molecular weight CC markers on Southern gels, and as chromosome markers or tags to identify concentration of immune deficiencies and disorders, such as severe combined CC immunedeficiency (SCID), as well as viral, bacterial, fungal and other infections. These infections include human immunodeficiency virus (HIV), CC candidiasis. The proteins can be used to treat autoimmune disorders such as connective tissue disease, multiple sclerosis, systemic lupus crythematosis, rheumatoid arthritis, autoimmune pulmonary inflammation, dislan-Barre syndrome, autoimmune thyroiditis, insulin dependent and arabitan arabitan arabitan arafilatis, autoimmune decleaned.
                                                                                                                                                                Query Match:
DB:
                                                                 Percent Similarity:
Best Local Similarity:
 US-10-001-254-26 (1-59)
                                                                                                                               Alignment Scores:
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                                                                                                                                                                  Sequence 5170
                                                                                                                                                                                                               diabetes mellitus, myasthenia gravis, graft-versus-host-disease autoimmune inflammatory eye disease. The proteins can also be us treat allergic conditions, such asthma. AAA16698 to AAA16774 rep
                                                                                                                   No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA16618 to AAA16697 encode the human secreted proteins given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides encoding secreted proteins, which may nutritional, chemokine, immune stimulating or suppressing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nutritional, chemokine, immune stimulating or suppressing, hematopolesis regulating, tissue growth, activin/inhibin antinflammatory or tumor inhibition activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1998
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04-SEP-1998;
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Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 590-592; 641pp; English
                                                                                                                                                                  BP;
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98US-0105368.
99US-0115234.
99US-0119931.
                                                                                                                                                                                             human secreted proteins from the present invention.
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99US-0096622
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Agostino MJ,
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4523 ATAGGTCTCATTAAACAGAGTGGAGATTTCATTGGTCAGCACTCCTCAATGAAA-----

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Sequence 349980 BP; 68046 A; 106490 C; 106389 G;

69055 T; 0 other;

Patent

Office.

ValGlyLeuIleArgLysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeu

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RESULT 13
ABQ81849
                                                                                           CC Sequences given in ABQ81843 and ABQ81843, or a sequence sqiven in CC (C least 90% identity or which hybridises with the sequence given in ABQ81842 and ABQ81843 as with the sequences given in CC ABQ81842 and ABQ81843. Also described is a polynucleotide (II) encoding CC a fusion protein, comprissing a sequence selected from 1097 sequences CC given in ABP65258 to ABP66354 ligated in frame to a polynucleotide (C antibacterial activities, and can be used as an inhibitor of Salmonella. (C (I) (which is a probe) is useful for the detection and/or identification CC of Bifidobacterium longum in a biological sample. A carrier containing CC the lactic acid bacterium sliftdobacterium longum NCC2705 (CNM 1-2618) (C can be used for preventing and/or treating diarrhoea brought about by CC pathogenic bacteria and/or rotavirus. The carrier is a food composition CC selected from milk, yogurt, curd, cheese, farmented milks, milk based CC fermented products, ice-creams, fermented cereal based products, milk based conders, infant formula, pet food or a pharmaceutical composition CC supplement, wet oral supplement, dry tube feeding or wet tube feeding. (I) is useful in DNA arrays or chips to carry out analysis of the C expression of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent CC listing from the present invention but not mentioned further within the constraint of the products of the Bifidobacterium but not mentioned further within the
   N.B. The sequence data for specification but is based
                                                                                specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotide comprising Bifidobacterium genome sequence useful as a probe or primer for detecting and/or identifying Bifidobacterium longum in a biological sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID 1105; 80pp; English
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identification; lactic acid bacterium; diarrhoea; pathogenic bactorium; diarrhoea; pathogenic bactorium; food composition; gharmaceutical composition; gene; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention describes a polynucleotide (I) comprising
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is not represented in the printed information supplied by the
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                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                genes from Drosophila and interactions
                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                  The sequence data for this patent did not form specification, but was obtained in electronic i
                                                                                                                                                                     Claim 1; SEQ ID NO 35386; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                               WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                      Venter
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                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental
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                      ftp.wipo.int/pub/published_pct_sequences.
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Alignment Scores

Sequence 3610

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RESULT 15
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                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABC07737-ABB72072).
                     The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                        New isolated nucleic a
genes from Drosophila
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11-JUL-2000; 2000US-0614150
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Search completed: January 18, 2004, 01:32:43 Job time : 98.7617 secs	.eLysLysProS :     ; :AACCCACCCGGTTF	.eArgLysLeuSer <i>l</i> :   :::   ::: TCGCCAGCTGGCA <i>I</i>	OlleThrProSerT	US-10-001-254-26 (1-59) x ABL27970 (1-3610)	24.7 66.00 52.73% 34.55% 20.43%
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	CASNGln 50	17 GlyLeuIleArgLysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAla     :::   :::   :::    2271 CAACTCCTTCGCCAGCTGGCAAAAGCGGAGGATGCCGGAAGTTCACAAGGTGGCT	2 ABBLYBProIleThrProSerThrTyrValArgCyBLeuABBVal		3610 19 10 20 6
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Title: Perfect score:

Scoring table:

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-MODELLEKTAME+ D21.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10001254/runat_16012004_152425_19740/app_query.fasta_1.1109
-Q=/cgn2_1/USPTO_spool/US10001254/runat_16012004_152425_19740/app_query.fasta_1.1109
-DB=Issued_Patents_NA -OPMT=fastap_-SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10001254 @CCN 1 1 95 @runat_16012004 152425_19740 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN _TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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APPLICANT: Chen, Yao
APPLICANT: Chen, Yao
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Jager, Elke
APPLICANT: Jager, Elke
APPLICANT: Jager, Elke
TITLE OF INVENTION: Wees Therefor
TITLE OF INVENTION: Uses Therefor
FILE REFERENCE: L0461/7051
CURRENT APPLICATION NUMBER: US/09/166,350A
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: US 09/166,350
EARLIER FILING DATE: 1998-10-05
NUMBER OF SEG ID NOS: 35
NUMBER OF SEG ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 833
                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
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; ORGANISM: Homo sapiens
US-09-166-350-10
                              US-10-001-254-26
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US-08-484-158B-21
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US-08-484-158B-21
US-08-484-158A-7
US-08-491-897A-7
US-08-674-887A-7
US-08-91-897-7
US-08-91-891-745
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US-09-599-564A-1
US-09-599-564A-6
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Result

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Length:
Matches:
Conservative:
Mismatches:
Indels:

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Gaps:

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Sequence 1, Application US/09009119

Patent No. 6160206

GENERAL INFORMATION:

APPLICANT: SATO, Ryo

APPLICANT: BOYNTON, John E.

TITLE OF INVENTION: Porphyrin Accumulating-Type Herbicide Res.

FILE REFERENCE: substitute sequence listing

CURRENT APPLICATION NUMBER: US/09/009,119

CURRENT FILING DATE: 1998-01-20

NUMBER OF SEQ ID NOS: 1

SOPTWARE: Patentin Ver. 2.0
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APPLICANT: Fraser et al.
TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma
Patent No. 6537773
TITLE OF INVENTION: Thereof, and Uses Thereof
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
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CURRENT APPLICATION NUMBER: US/08/545,528D
CURRENT FILING DATE: 1995-10-19
PRIOR APPLICATION NUMBER: US 08/488,018
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/473,545
PRIOR FILING DATE: 1995-06-07
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ORGANISM: Mycoplasma genitalium
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Query Match:
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; ORGANISM: Chlamydomonas reinhardtii
US-09-371-507-1
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Patent No. 6346656
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SATO, Ryo
APPLICANT: BOYNTON, John E.
APPLICANT: BOYNTON, John E.
APPLICANT: HARRIS, Elizabeth H.
TITLE OF INVENTION: Porphyrith Accumulating-Type He;
FILE REFERENCE: substitute sequence listing
CURRENT APPLICATION NUMBER: US/09/371,507
CURRENT FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: 09/009,119
PRIOR FILING DATE: 1998-01-20
INMBER OF SEQ ID NOS: 1
                                                                                                                                                     US-10-001-254-26 (1-59) x US-09-371-507-1 (1-3381)
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36 AlaValAlaIleLysLysProSerGlyAspAspArgTyrAsnGlnPheHisIleArgCys
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                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DN
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CURRENT APPLICATION DATA:
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ORGANISM: Chl
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MEDIUM TYPE: Floppy disk
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APPLICANT: Gillham, licholas W.
APPLICANT: Harris, Elizabeth H.
TITLE OF INVENTION: Porphyrin-Accumulating Type Herbicide
TITLE OF INVENTION: Resistance Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                               STRAIN: RS-3
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Best Local Similarity:
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                                                                                                                         SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09111085 Patent No. 6100034 GENERAL INFORMATION:
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LENGTH: 1182
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                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/111,085
CURRENT FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: GB 9710154.7
EARLIER FILING DATE: 1997-05-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                TITLE OF INVENTION: Detection of retroviral subtypes based upon envelope TITLE OF INVENTION: specific sequences FILE REFERENCE: 4238/75168
                                                                                                                                                                                                                                                                                                                            APPLICANT: Stoye, Jonathan P
APPLICANT: Weiss, Robin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MAIC J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
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                                                     LENGTH: 3482
TYPE: DNA
ORGANISM: Porcine retrovirus
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ORGANISM: Pseudomonas
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Best Local Similarity:
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                                                                                                                Sequence 9, Application US/08123934A Patent No. 6291206
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 202001
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APPLICANT: WEI, Ming-Hui et al
APPLICANT: WEI, MING-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUN
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001018
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Patent No. 6498022
GENERAL INFORMATION:
APPLICANT: WOZNEY, John
APPLICANT: CELESTE, Anthony J.
APPLICANT: THIES, R. Scott
APPLICANT: YAMAJI, No. 6291206oru
TITLE OF INVENTION: RECEPTOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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PCT-US94-10080-9/c
; Sequence 9, Application PC/TUS9410080
; GENERAL INFORMATION:
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Best Local Similarity:
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REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/123,934A
FILING DATE: 17-SEP-1993
CLASSIFICATION: 530
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ADDRESSEE: Genetics Institute Inc.- Legal Affairs
ADDRESSEE: 87 CambridgePark Drive
                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute Inc.- Legal Affairs STREET: 87 CambridgePark Drive
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                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                     TITLE OF INVENTION: RECEPTOR PROTEINS
                                                                                                                                       APPLICANT:
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LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                  CITY:
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COUNTRY:
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617 876 5851
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Best Local Similarity:
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                                                                                                                                                                                            Sequence 1, Application US/07923976 Patent No. 5574136
                                                                                                                                                                              GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
STREET: P.U. STREET: VIrginia
                                                         NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: Jones, Tu
                                                                                                            TITLE OF INVENTION:
                                                                                                                                        APPLICANT: Nagata, Shigekazu
APPLICANT: Fukunaga, Rikiro
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IMMEDIATE SOURCE:
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TELEPHONE: (617) 498-8260
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CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
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CLASSIFICATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                           1467 TCACAGCTCTGCCATCTGTTTGGAATATTTGGCCTTAACTTCTGTTCGCAA 1417
                                                                                                                                                                                                                                                                                                                                             1527 CTTGCTGCTCCATTGGCATACCAGCATTCTCTCATAATTTTAGCCATCACTCTCAAGGCC 1468
                                                                                                                                                                                                                                                                                                                                                                                                             1587 TIGATGCCTTCCTGTTGGCTGAGTTGTGACAATGTTTTTTTAATTCGCAAAGCTGTCAGC 1528
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                                                                                                                                                                                                                                                                                                                                                                           25 PheIleAspPro------GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLys 41
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                                           E: Jones, Tullar & Cooper, P.C.
P.O. Box 2266 Eads Station
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83..1591
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57.50
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31.58%
17.80%
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Best Local Similarity:
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                                               GENERAL INFORMATION:
APPLICANT: Stoye, Jonathan P
APPLICANT: Weiss, Robin A
                                                                                                   Sequence 1, Application US/09111085 Patent No. 6100034
TITLE OF INVENTION: Detection of retroviral subtypes based upon envelope TITLE OF INVENTION: specific sequences FILE REFERENCE: 4238/75168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 703-415-1508
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: JP 7
FILING DATE: 23-MAR-1990
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LOCATION:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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28.36%
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Conservative:
Mismatches:
Indels:
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APPLICANT: POTTBUTY, Stuart D.
APPLICANT: PUTTBUTY, STUART D.
APPLICANT: RATZ, LAWTENCE C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: COMPOSITIONS CONDITIONS,
TITLE OF INVENTION: COLL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 402
LENGTH: 936
TYPE: DNA
ORGANISM: Homo Sapiens
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US-09-461-697-402
                                                Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-001-254-26 (1-59) x US-09-461-697-402 (1-936)
                                                                                                      Score:
                                                                                                                     Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence 402, Application US/09461697 Patent No. 6277974 GENERAL INFORMATION:
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CURRENT FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: US 9710154.7
EARLIER FILING DATE: 1997-05-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 2462
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart
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57.00
39.34%
31.15%
17.65%
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56.50
31.46%
23.60%
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                                              Conservative: Mismatches: Indels:
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Matches:
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Matches:
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APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AN
TITLE OF INVENTION: COMPOSITIONS AN
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 396
LENGTH: 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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262 ACCGAAGCACTAGATAATGTTCTGAAATACCTCCCAAAA-----AAGGATCGAGAA 312
                                                                                                                                              142
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                                29 GlnGluGlyTrpLysLysLeuAlaValAlaIleLysLysProSerGlyAspAspArgTyr 48
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                                                                                                                                              CCCATCATGGAGACATTCTTAAGTAAAGCGCGTCTTCCTCTTGGAGCTACCAGTTCTAAA 201
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Matches:
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APPLICANT: POTTBUTY, Stuart D.
APPLICANT: POTTBUTY, STUART
APPLICANT: Natz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: COMPOSITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 394
LENGTH: 1128
TYPE: DNA
ORGANISM: Homo sapiens
US-09-461-697-394
Search completed: January 18, 2004, 06:11:39 Job time : 73.3955 secs
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US-09-461-697-394
US-09-461-697-394
; Sequence 394, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: COGENT NEUROSCIENCE, Inc. APPLICANT: Lo, Donald C. APPLICANT: Barney, Shawn APPLICANT: Thomas, Mary Beth
                                                                                                                                                  373 ACCGAAGCACTAGATAATGTTCTGAAATACCTCCCAAAA---
                                                                                                                                                                                                                            313 GGGAGGAGACACCACCGAATCCTGGGACTTCTGAATTGGTTGTCTCATTTTGCCAACCCT 372
                                                                         424 AATGTTAAGGAACTTCTCTGCTGTTCC 450
                                                                                                                                                                                                                                                                                                                                                                                   193 ATGAATAAAGCTCTACTACCTCTCTTTGCGGTGCTATGTGGGAAATGACCATGTTAATCTA 252
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                                                                                                           AsnGlnPheHisIleArgCysCysSer 57
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Matches:
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Result
No.
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-Qc/cgn2 1/USPTO spool/US10001254/runat 16012004 152426 19815/app_query.fasta_1.1109
-Qc/cgn2 1/USPTO spool/US10001254/runat 16012004 152426 19815/app_query.fasta_1.1109
-DB=PublIshed Applications NA -QFMT-fastap -SUFFTX=rmpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIXED-bosum62
-TRAMS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10001254 @CGN 1 1534 @runat 16012004 152426 19815
-NCPU=6 -ICPU=3 -NO MMAP -LARGSQUERY -NEG SCORES=0 -WAIT -DSEPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
              Score
                                                                                                                                                                                                                                                                                        Published Applications NA:*

1: /cgn2_6/ptcdata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptcdata/1/pubpna/USO6_NEW_PUB.seq:*

3: /cgn2_6/ptcdata/1/pubpna/USO6_NEW_PUB.seq:*

4: /cgn2_6/ptcdata/1/pubpna/USO6_PUBCOMB.seq:*

5: /cgn2_6/ptcdata/1/pubpna/USO7_NEW_PUB.seq:*

6: /cgn2_6/ptcdata/1/pubpna/USO7_NEW_PUB.seq:*

7: /cgn2_6/ptcdata/1/pubpna/USO8_NEW_PUB.seq:*

8: /cgn2_6/ptcdata/1/pubpna/USO8_PUBCOMB.seq:*

9: /cgn2_6/ptcdata/1/pubpna/USO8_PUBCOMB.seq:*

10: /cgn2_6/ptcdata/1/pubpna/USO9B_PUBCOMB.seq:*

11: /cgn2_6/ptcdata/1/pubpna/USO9B_PUBCOMB.seq:*

12: /cgn2_6/ptcdata/1/pubpna/USO9_NEW_PUB.seq:*

13: /cgn2_6/ptcdata/1/pubpna/USO9_NEW_PUB.seq:*

14: /cgn2_6/ptcdata/1/pubpna/USO9_NEW_PUB.seq:*

15: /cgn2_6/ptcdata/1/pubpna/USO9_NEW_PUB.seq:*

16: /cgn2_6/ptcdata/1/pubpna/USO9_NEW_PUB.seq:*

16: /cgn2_6/ptcdata/1/pubpna/USO9_NEW_PUB.seq:*

17: /cgn2_6/ptcdata/1/pubpna/USO0_NEW_PUB.seq:*

16: /cgn2_6/ptcdata/1/pubpna/USO0_NEW_PUB.seq:*

17: /cgn2_6/ptcdata/1/pubpna/USO0_NEW_PUB.seq:*

18: /cgn2_6/ptcdata/1/pubpna/USO0_NEW_PUB.seq:*
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Ygapop 10.0 , Ygapext
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Query
Match Length DB
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323
1 MNKPITPSTYVRCLNVGLIR.....KKPSGDDRYNQFHIRCCSQN
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Listing first 45 summaries
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                                                                                                                SUMMARIES
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2 290 89.8 1383 11 US-10-001-254-25 Sequence 25, Appli 329 89.8 1383 11 US-00-975-595-2 Sequence 2, Appli 3290 89.8 2817 11 US-10-01254-15 Sequence 2, Appli 5290 89.8 2817 11 US-10-01254-27 Sequence 27, Appli 5290 89.8 2817 11 US-10-01254-27 Sequence 27, Appli 5290 89.8 2817 15 US-10-01254-27 Sequence 27, Appli 6290 89.8 31000 11 US-09-966-451-10 Sequence 27, Appli 727 85.8 291 91 US-10-01254-5 Sequence 27, Appli 8291 142 11 US-09-795-95-4 Sequence 27, Appli 8291 142 11 US-09-795-95-4 Sequence 57, Appli 142 17 32.6 497 14 US-10-027-632-50723 Sequence 50724, Appli 142 17 32.6 497 14 US-10-027-632-50723 Sequence 50724, Appli 142 17 32.6 499 12 US-10-027-632-72567 Sequence 72567, Appli 72 26 499 12 US-10-027-632-72567 Sequence 72568, Appli 15 US-10-027-632-72567 Sequence 72568, Appli 16 73 22.6 499 12 US-10-027-632-72567 Sequence 72568, Appli 16 73 22.6 499 12 US-10-027-632-72567 Sequence 72568, Appli 17 US-10-027-632-72567 Sequence 72568, Appli 18 2488 13 US-10-027-632-72568 Sequence 230, Appli 66 211 18 170 11 US-09-374-046, 131 Sequence 630, Appli 18 2488 13 US-09-870-133-1 Sequence 630, Appli 18 2488 13 US-09-870-133-1 Sequence 64, Appli 18 2488 13 US-09-870-133-1 Sequence 64, Appli 18 2488 13 US-09-870-133-1 Sequence 64, Appli 18 2488 13 US-09-870-133-1 Sequence 156804, Appli 64 19.8 2338 13 US-09-870-133-1 Sequence 156803, Appli 64 19.8 2338 13 US-09-870-133-1 Sequence 156804, Appli 64 19.8 2338 13 US-09-870-133-1 Sequence 156803, Appli 64 19.8 2338 13 US-09-870-873-156803 Sequence 156804, Sequen
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## ALIGNMENTS

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RESULT 1
US-10-001-254-25

Sequence 25, Application US/10001254

Publication No. US20030049702A1

GENERAL INFORMATION:

APPLICANT: Reed, John C.

APPLICANT: Godzik, Adam

APPLICANT: Howelowski, Krzysztof

APPLICANT: Lee, Sug Hyung

APPLICANT: Lee, Sug Hyung

APPLICANT: Stenner-Liewen, Frank

TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins

FILE REFERENCE: P-LJ 5037

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/715,893

PRIOR APPLICATION STENCE: 99/715,893

PRIOR APPLICATION DATE: 2000-11-17

NUMBER: OF SEQ ID NOS: 62

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 25

LENGTH: 211
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                                                                                                                                                                                                    Score:
                                                                                                                                                                                                                                                             NAME/KEY: CDS
; LOCATION: (1)..(1383)
; OTHER INFORMATION: human
US-09-759-595-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-001-254-26 (1-59) x US-10-001-254-25 (1-211)
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Best Local Similarity:
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US-10-001-254-25
                                                                                                  US-10-001-254-26 (1-59) x US-09-759-595-2 (1-1383)
                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09759595 Publication No. US20030059916A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wesche, Holger
APPLICANT: Li. Shyun
APPLICANT: Li. Shyun
APPLICANT: Tularik Inc.
TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use
FILE REFERENCE: 018781-003910US
CURRENT APPLICATION NUMBER: US/09/759,595
CURRENT FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapien FEATURE: NAME/KEY: CDS LOCATION: (1)...(177)
                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: human IL-1 receptor-associated kinase 4 (IRAK-4) OTHER INFORMATION: cDNA
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AAACCATCTGGTGATGATAGATACAATCAGTTTCACATAAGATGCTGTTCCCAAAAC 177
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LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLys
                                                      MetAsnLysProIleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg
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Sequence 3, Application US/09966451
Publication No. US20030087856A1
GENERAL INFORMATION:
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APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLB OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
FILE REFERENCE: RTS-0324
CURRENT APPLICATION NUMBER: US/09/366,451
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 15
LENGTH: 1383
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ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1380)
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TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins
FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-6-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
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SOFTWARE: FastSEQ for Windows Version
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Pawlowski, Krzysztof
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No. US20030049702A1
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Roth, Wilfred
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US-10-001-254-27
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US-09-966-451-3
                                               US-10-001-254-26 (1-59) x US-10-001-254-27 (1-2817)
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US-10-001-254-27
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                                                                                                                                                                                                                                                                                                    SEQ ID NO 27
LENGTH: 2817
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CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
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APPLICANT: God:
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NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows
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TITLE OF INVENTION: No. US20030049702Alel Death Domain Proteins
FILE REFERENCE: P-LJ 5037
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                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo
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MetAsnLysProIleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg
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Fiorentino, Loredana
Lee, Sug Hyung
Roth, Wilfred
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US-09-833-790-149
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APPLICANT: Wang, Tongtong
APPLICANT: Secrist, Heather
APPLICANT: Mohamath, Raodoh
APPLICANT: Indirias, Carol Y.
APPLICANT: Fan, Liqun
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                                                             SEQ ID NO 149
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                                                                                                                           APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
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APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRES
FILE REFERENCE: RTS-0324
CURRENT APPLICATION NUMBER: US/09/966,451
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 88
                                                                                    NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
ORGANISM: Homo sapien
                      TYPE: DNA
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Query Match:
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                                                                                                                      US-10-001-254-26 (1-59) x US-09-759-595-4 (1-1542)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 4
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APPLICANT: Tularik Inc.
TITLE OF INVENTION: IRAK-4: Compositions and
FILE REFERENCE: 018781-003910US
CURRENT APPLICATION NUMBER: US/09/759,595
CURRENT FILING DATE: 2001-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
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OTHER INFORMATION: n = A, T, C
                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (163)..(1542)
OTHER INFORMATION: murine IRAK-4
                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4)
                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus sp.
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                                                   163 ATGAACAAGCCGTTGACACCATCGACATACGTAACCTTAATGTGGGGATCCTTAGG
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LysLeuSerAspPheIleAspProGlnGluGlyTrpLysLysLeuAlaValAlaIleLys
                                                                      MetAsnLysProIleThrProSerThrTyrValArgCysLeuAsnValGlyLeuIleArg
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90.74%
83.90%
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277.00
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Matches:
Conservative:
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Indels:
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US-10-027-632-50723/c
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US-10-001-254-5
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          Sequence 50723, Application US/10027632
publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR RILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
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SEQ ID NO 5
LENGTH: 294
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
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Publication No.
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CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
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TITLE OF INVENTION: No. US20030049702Alel Death Domain
FILE REFERENCE: P-LJ 5037
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PRIOR APPLICATION NUMBER: US 60/198,676
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                                                                                                                                                                                                                                                                                                  121 AATCAGTTTCACATAAGG 138
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No. US20030049702A1
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Alignment Scores: Pred. No.:
                                                                                ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-50724
                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1090-10-360/185,218
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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US-10-027-632-50723
                                                                                                                                                                    SOFTWARE: Fast
SEQ ID NO 50724
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TITLE OF INVENTION: Identification
TITLE OF INVENTION: Polymorphisms
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PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
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OS: 325720
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RESULT 13
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Best Local Similarity:
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Best Local Similarity:
Sequence 50724, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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FILING DATE: 2000-07-12
APPLICATION NUMBER: US 60/198,676
FILING DATE: 2000-04-20
APPLICATION NUMBER: US 60/193,483
FILING DATE: 2000-03-29
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30

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; ORGANISM: Human
US-10-027-632-50724
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SOFTWARE: FastSEQ for
SEQ ID NO 72567
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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ORGANISM: Human
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FILING DATE: 2000-04-20
APPLICATION NUMBER: US 60/193,483
FILING DATE: 2000-03-29
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FILING DATE: 1999-11-23
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US-10-027-632-72568/c
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US-10-027-632-72568
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR TILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-09-28
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PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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SEQ ID NO 72568
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CURRENT FILING DATE: 2002-04-30
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BG616438 602642772
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Homo sapiens (human)
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CONMENT
Email: cgapbs-remail.nih.gov/
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CONALIBRATY Preparation: MGC clone distribution can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10240 row: d column: 08
High quality sequence stop: 634.

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                                                  CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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BG616438.1 GI:13667809
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602642772F1 NIH_MGC_61 Homo sapiens
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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                      CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov hlate: LLCM124 row: g column: 15
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Tissue Procurement: ATCC
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602130160F1 NIH_MGC_56 Homo sapiens
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/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_61"
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SfiI (ggccgctcgggc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCGATMINGGCC-3' and 3' adaptor sequence: 5'-CACGGCCGATMINGGCC-3' and 3' adaptor sequence: 5'-CATGCCGACATMINGGCC-3' and 3' adaptor sequence: 5'-CATGCCGACATMINGCC-3' and 3' adaptor sequence: 5'-CATGCTAMINGCC-3' and 3' adaptor sequence: 5'-CATGCCGACATMINGCC-3' and 3' adaptor sequence: 5'-CATGCCGACATMINGCC-3' and 3' adaptor sequence: 5'-CATGCCGACATMINGCC-3' and 3' adaptor sequence: 5'-CATGCTAMINGCC-3' and 3' adaptor sequence: 5'-CATGCCGACATMINGCCC-3' and 3' adaptor sequence: 5'-CATGCCCGACATMINGCCC-3
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99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 292.4; DB 10;
Pred. No. 4.4e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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cDNA clone IMAGE:4287014 5',
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                                                                                                                                                                                                                                                                                                                                                                                  Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316
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RESULT 4
BE482619
LOCUS
DEFINITION
ACCESSION
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AUTHORS
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ORGANISM
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ORIGIN
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                                                                MEDLINE
PUBMED
                                                                                                                             TITLE
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Best Local Similarity
                                                                                               JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
                                                                                                                                                                                                                                                                                    BE482619 402 bp mF
168463 BARC 5BOV Bos taurus cDNA 5',
BE482619 BE482619.1 GI:9602152
EST.
                                                                                                                                                       Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D. a.
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                       Bos taurus (cow)
                                                                                                                         Analysis of bovine mammary gland EST
                                                                12140684
                                                                                22135956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAATTACT-GTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTTTT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATCCAAAATGAATTT-TTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 151
                                                                                                                                                                                                                                                                                                                                                                                                                               GATCCAAAATGAATTTGTTGGCTCCTGCAAGTCTTTTGCTCCCAGATGCTGTTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATCAGTTTCACATAAGGAGTTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT 271
                                                                                                                                                                                          (bases 1 to 402)
                                                                                        Bos taurus gene index
m. Genome 13 (7), 373-379 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="primitive neuroectoderm"
/lab host="PH10B (T1 phage-resistant)"
/clone_lib="NH10B (T1 phage-resistant)"
/clone_lib="NH1MGC_56"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ANTCTAGAGGCCGAGGCGCGCACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:4287014"
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Pred. No. 4.8e-64;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                 mRNA linear
', mRNA sequence.
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                                                                                                                                                                        Connor, E.E.
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                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                   RESULT 5
BG691069
LOCUS
DEFINITION
ACCESSION
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ORIGIN
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                                              MEDLINE
                                                           JOURNAL
                                                                                            TITLE
                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                       EST
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1 (bases 1 to 541)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D. au
Quackenbush, J.
Analysis of bovine mammary gland EST and functional anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541 bp
340084 BARC 5BOV Bos taurus cDNA
BG691069
BG691069.1 GI:13932889
EST.
Contact: Sonstegard TS USDA, ARS, Beltsville
                                                                                                                                                             the Bos taurus gene index Mamm. Genome 13 (7), 373-379
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACKWARD: GTTTTCCCAGTCACGACG
Plate: 11 row: F column: 7
Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                           22135956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 301 504 8414
                                                                            2140684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCCAAAATGAGTTTTTTTGCCCCTGCAAGTCTTTTGCTACCAGATGCTGTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGTTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATATTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACATATGTGCGCTGCCTCAATGTTGGACTAATTTAGGAAGCTGTCAGATTTTTATTGATCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -minmatch 12 options.
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/lab host="PH10B"
/lab host="PH10B"
/clone lib="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sall;
/note="Type to the state of the state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Bos taurus"
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93.2%;
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Agricultural Research Center
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Pred. No. 1.1e-62;
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AUTHORS
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ORGANISM
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KEYWORDS
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BM151935
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Best Local Similarity
                                                                            TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases call
v0.980904.e. Vector identified by
                                                                                                                                                                                                                                                                                                                 BM151935
313 bp mRNA linear EST 30-NOV TCBAP1E11457 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP1145, mR
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PCR PRimers
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Tel: 301 504 8416
Fax: 301 504 8414
                  Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center a
                                                        Unpublished
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                        Gunaratne, P.H., Muzny, D., Bouck, J., Gibbs, I
Pediatric Leukemia cDNA Sequencing Project
                                                                                                              Wei, Y., Tsang, Y.T.M., Mei, G.,
                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                           BM151935.1 GI:17175815
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                                                                                                                                                                                                                    Homo sapiens (human)
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Baylor College of Medicine
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primer: ATTTAGGTGACACTATAG.
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/tissue_type="pooled"
/lab_host="DH10B"
/lab_host="DH10B"
/clone_lib="BARC_SBOV"
/clone_lib="BARC_SBOV"
/note="Vector: pCMV_SPORT6; Site_1: NotI; Site_2: SalI;
Library_made_from_pooled_mRNA_isolated_from_mammary_
tissues_at_eight_physiological,_developmental,_and_dises_
states_"
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/mol_type="mRNA"
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93.9%;
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                    and Human
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                                                                                             M., Ali-Osman, F.R. Jr., Gibbs, R.A. and Margolin, J.
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C0272B01-5N NIA Mouse 7.5-dpc Whole Embryo cDNA Library (Long) Mus musculus cDNA clone NIA:C0272B01 IMAGE:30017484 5', mRNA sequence. CA538859

CA538859.1 GI:25080828
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Piao, Y., Kargul, G.J., Dudekula, D.B.,
Luo, A. and Ko, M.S.H.
Systematic Analyses of NIA Mouse 7.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@txc
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 503)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13 primer
                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1102 Bates, MC3-3320 Houston,
                                                                                                                                                   Mus musculus (house mouse)
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//dev stage="pediatric 2 years"
//lab host="DH108"
//clone_lib="Pediatric pre-B cell acute lymphoblastic
leukemia Baylor-HGSC project=TCBA"
//note="Yector: lambda pSB; Site 1: BamHI; Site 2: EcoRI;
//note="Yector: lambda pSB; Site 1: BamHI; Site 2: EcoRI;
//note="Yector: lambda pSB; Site 1: BamHI; Site 2: EcoRI;
//note="Yector: lambda pSB; Site 1: BamHI; Site 2: EcoRI;
//note="Yector: lambda pSB; Site 1: BamHI of the nation of strand cDNA was primed with an anchored -
XhoI-oligo(dT) primer [5/GGAGGAGCGCGCAATAATAATAATAAT(C) 3'].

[5/AGAGAGCTCGGAGTCCGCGCGCCAATAATAATAAT(C) 3'].

Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramateu M, Schneider C, Hayashizaki Y, Hish efficiency selection of full-length cDNA by improved biotinylated cap trapper.,
DNA Res 4: 1, 61-6, Feb 28, 1997)"

82 a 62 c 81 g 87 t 1 others
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/cell_type="pre-B cell"
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|mol_type="mRNA"
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clone="TCBAP1145"
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      of NIA Mouse 7.5-dpc Whole Embryo cDNA Library
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                                             Qian,Y.,
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                                                                                        Murinae;
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Plate: C0272 row: B column: 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
Other_ESTs: C0272B01-3
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ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 294
                                                                                 GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG
                                                                                                                                                                                                                                                                                                 ACATACATACGCAACCTTAATGTGGGGATCCTTAGGAAGCTGTCGGATTTTATTGATCCT
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                                       GAACTGCTGTTTGACTGGGGCACCACGAACTGCACAGTTGGCGACCTTGTGGATCTACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed by Yulan Piao (NIA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pSPORT1 (Invitrogen); Site 1: Sal1; Site 2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of four embryos at 7.5-days
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="whole embryo including extraembryonic
tissues at 7.5-days postcoitum"
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/lab_host="DH10B"
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Pred. No. 1.6e-46;
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Best Local Similarity
356
                                                    181 GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTTTTG
                                                                                                                                                                                                                                                 121 AATCAGTTTCACATAAGGAGTTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
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Laboratory of Genetics
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
Plate: H4014 row: C column: 09
Seg primer: -21M13 Reverse
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Mammalia; Eutheria; Rodentia;
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GAACTGCTGTTTGACTGGGGCACCACGAACTGCACAGTTGGCGACCTTGTGGATCTACTG
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/lab_host="DH10B"
/lab_nost="DH10B"
/clone lib="NIA Mouse 7.4K cDNA Clone Set"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
/note="Vector: pSPORT1; Site_1: SalI; Site_1: SalI; Site_2: NotI; This
/note="Vector: pSPORT1; Site_1: SalI; Site_1: SalI; Site_2: NotI; This
/note="Vector: pSPORT1; Site_1: SalI; SalI
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Hamatani,T., Kargul,G.J.,
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RESULT 9
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1 (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
uavashiari
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB660378 linear BB660378 RIKEN full-length enriched, 13 days embr musculus CDNA clone D430042L21 5', mRNA sequence. BB660378 BB660378.1 GI:16494199 EST.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computational Analysis of Full-Length Mouse cDNAs Compared with fuman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissues.
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                     organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                  dev_stage="13 days embryo"
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                    ATCCAAAATGAATTTTTTTGCTCCTGCGAGTCTTTTTGCTCCCAGATGCTGTTCCC
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                                                                                         GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGGATCTTTTG
                                                                                                                                            AATCAGTTCCATATAAGGAGATTCGAAGCCTTACTTCAGACCGGGAAGAGCCCCCACCTGT
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                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primed with a primer [5'
                                                                                                                                                                                                                                                                                                                                                                            69.5%;
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REFERENCE
AUTHORS
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1 (bases 1 to 637)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara Hramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kc, M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sae,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., D., Shibata,K., Shinagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB613447 637 bp mRNA linear BB613447 RIKEN full-length enriched, 10 day neona musculus cDNA clone 4732482P03 5', mRNA sequence. BB613447
                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                           Tel: 81-45-503-9222 Fax: 81-45-503-9216
                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
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                                                                                1-7-22 Suehiro-cho, Tsurumi-ku,
genome-res@gsc.riken.go.jp
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                                                                                230-0045, Japan
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                                                                                                                               61
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Konno, H., Fukunishi, Y. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computer-based methods for the mouse full-length cDNA
                                                                                                             ACATACATACGCAACCTTAATGTGGGGGATCCTTAGGAAGCTGTCGGATTTTATTGATCCT
                                                                              CAAGAAGGGTGGAAGAATTAGCAGTAGCTATCAAAAAGCCGTCCGGCGACGACAGATAC
                                                                                                                                                                                                                                                                                                                                                                                                           162
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           ρ
                                                                                                                                                                                                                                                                                                                                                                                                contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="skin"
/dev_stage="10 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="RIKEN full-length enriched, 10 day neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Site_1: Sall; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="4732482P03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xref="taxon:10090"
                                                                                                                                                                                                                                                                                                        69.5%;
                                                                                                                                                                                                                                                                                 <u>,</u>
                                                                                                                                                                                                                                                                                                        Score 204.4;
Pred. No. 1.8
                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                   .8e-46;
                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                 56;
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                               637;
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                                                                                                                               120
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JOURNAL MEDLINE PUBMED COMMENT RESULT 11 BY721552 VERSION KEYWORDS LOCUS DEFINITION REFERENCE SOURCE 밁 S 밁 8 ACCESSION TITLE AUTHORS ORGANISM Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldareili, R., Hill, D. P., Bull, C., Hume, D. A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Gorbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, R.J., Kanabe, G., Wandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wall, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Wallana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Yang, I., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., M., Yang, I., Yang, L., Zavolan, M., Zhu, Y., Zimmer, A., M., Yang, I., Myazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shihata, Y., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Blin, C., Mang, Y., Mang, S., Shibata, Y., Shibata 373 313 AATCAGTTCCATATAAGGAGATTCGAAGCCTTACTTCAGACCGGGAAGAGCCCCCACCTGT 372 433 GTCCAGATTGAGCTGTTTGCCCCCCCCCACTCTCCTGCTGCCGGATGCCGTTCCC 241 AFCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 294 Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohasto,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct BY721552 BY721552 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jag-191: 81-45-503-9222 Contact: Yoshihide Hayashizaki 12466851 Okazaki, Y., Furuno, M., Mus musculus Fax: 81-45-503-9216 22354683 Eukaryota; BY721552.1 musculus cDNA Mus musculus (house mouse) Computational Analysis of Full-Length Mouse cDNAs Compared with GAACTGCTGTTTGACTGGGGCACCACGAACTGCACAGTTGGCGACCTTGTGGATCTACTG GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG 240 (bases 1 to 638) 638 bp mRNA linear EST 17-DE RIKEN full-length enriched, adult male diencephalon cDNA clone 9330209D03 5', mRNA sequence. ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Kasukawa, T., Adachi, J., Bono, H., EST 17-DEC-2002 Kondo,S., 486 Mus 432

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

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438 GTCCAGATTGAGCTGTTTGCCCCCCGCCACTCTCCTGCTGCCGGATGCCGTTCCC 491

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
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241 ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 294
                                                                   378
                                                                                                           181
                                                                                                                                                    318
                                                                                                                                                                                              121
                                                                                                                                                                                                                                     258 CAAGAAGGGTGGAAGAATTAGCAGTAGCTATCAAAAAAGCCGTCCGGCGACGACAGATAC
                                                                                                                                                                                                                                                                                                                        198
                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                           238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome CRs. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-
sequencing pipeline with 384 multicapillary sequencer.
10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             further
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                         GAATTACTGTTTGACTGGGGCACCACAAATTGCCACAGTTGGTGATCTTTTG
                                                                                                                                                                                                                                                                 AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
                                                                   GAACTGCTGTTTGACTGGGGCACCACGAACTGCACAGTTGGCGACCTTGTGGATCTACTG
                                                                                                                                                    AATCAGTTCCATATAAGGAGATTCGAAGCCTTACTTCAGACCGGGAAGAGCCCCCACCTGT
                                                                                                                                                                                                                                                                                                                        ACATACATACGCAACCTTAATGTGGGGATCCTTAGGAAGCTGTCGGATTTTATTGATCCT
                                                                                                                                                                                                                                                                                                                                                             ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand CDNA was primed with a primer [5' GAGAGAGAGAGAGCTCTTTTTTTTTTTTTTTVN 3'], CDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BamHI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diencephalon"
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[0]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="9330209D03"
                                                                                                                                                                                                                                                                                                                                                                                                                          69.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _stage="adul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lib="RIKEN full-length enriched, adult male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type="diencephalon"
                                                                                                                                                                                                                                                                                                                                                                                                         <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                       Score 204.4; DB 14
Pred. No. 1.8e-46;
0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117
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                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  638;
                                                                                                                                                                                                                                                                                                                                                                                                       0;
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COMMENT

Contact: Yoshihide Hayashizaki

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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222 Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Hori,F., Imotani,K.,
S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno
H., Koya,S., Miyazaki,A., Murata,M., Nemura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. 10 (11), 1757-1771 (2000)

Res.

for the mouse full-length cDNA

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RESULT 12
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                                                                                                                               TITLE
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                     Nikaido, I., Osato, N., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Yagi, K., Bake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Cusins, S., Dalla, E., Dragani, T.A., Fletcher (C.F., Forrest, K.E., Cousins, S., Dalla, E., Dragani, T.A., Hetcher (C.F., Forrest, A., Frazer, K.S., Gassterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Yaryis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Wing, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchiomi, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringdala, K., Schneider, C., Semple, C.A., Setou, M., Sahga, K., Shitana, R., Takenaka, Y., Taylor, M.S., Tesdale, R.B., Yang, I., Yang, L., Yang, L., Yang, L., Yang, L., Yang, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Waltsu, N., Hirozane-Kishikawa, T., Komno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Kayawa, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Nakamura, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Nakai, K., Sasaki, D., Shibata, K., Shiraki, Y., Ishii, Y., Ithin, Shibata, Y., Shibata, Y.
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22354683
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                               BB613167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                              GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTTTGGGATCTTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                   CAAGAAGGGTGGAAGAAATTAGCAGTAGCTATCAAAAAGCCCGTCCGGCGACGACAGATAC
                                                                                                                                                                          GTCCAGATTGAGCTGTTTGCCCCCGCCACTCTCCTGCTGCCGGATGCCGTTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                   676 bp mRNA RIKEN full-length enriched, 10 cDNA clone 4732460109 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research foroup in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified pBluescript KS(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contributed to prepare
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/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mkwa"
/db_xref="taxon:10090"
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wagi,K., Fujiwake,S., Inoue,K., Togawa,K., Tanaka,T., Matsuu
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizaw,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Genome Sequences. Mamm. Genome. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing pipeline with 384 multicapillary se
10 (11), 1757-1771 (2000)
Konno, Fukunishi,Y., Shibata,K., Itoh,M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computer-based methods for the mouse full-length cDNA
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                                                                                     /note="Site 1: Sal1; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]
                              prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-lend
                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="skin"
/dev_stage="10 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mol_type="mRNA"
|strain="C57BL/6J"
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Rodentia;
subsequently enriched for full-length by went through one round of normalization
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nizaki,Y.
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          Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Mateuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                     Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AK020397
AK020397.2 GI:15919911
HTC; CAP trapper.
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1161 bp mRNA linear HTC 05-DEC-2002 Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330209D03 product:interleukin-1 receptor-associated kinase 4 [Mus musculus], full insert sequence.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1161)
                                                                                                                                                                                       Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-Coi. Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Oct 4, 2001 this sequence version replaced gi:12860970 Please visit our web site (http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
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                             BamHI and XhoI. Vector: a modified pBluescript excision from Lambda FLC I. Cloning sites, 5' e BamHI. Host: DH10B.
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Adachi,J.,
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                                                                                                                              Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to
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AK028837
AK028837.1 GI:26324783
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2481 bp mRNA linear HTC 05-DEC-2002
Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
library, clone:4732460109 product interleukin-1 receptor-associated
kinase 4 [Mus musculus], full insert sequence.
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SDTRFHSFSFHELKSITNNFDEQPASAGGNRMGEGGF"
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183. ..776
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receptor-associated kinase 4 [Mus musculus]
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2481)
                                                                                                                                                                                     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN enders Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishin,K., Kitsunai,T., Tashico,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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receptor-associated kinase 4 [Mus musculus]
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/clone_llb="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10 days neonate"
116._.1495
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/strain="C57BL/6J"
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3. /SIDS1/gcgdata/genesed/geneseqn-embl/NA1982.DAT:*

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ABV47522	ABV47458	ABV17729	ABV17967	AAT94064	AAN91323	AAH54085	ABZ34930	AAX99301	ABS52506	AAI99855	AAI99844	AAC27964	ABA92787	AAH42107	ABN66233	ABZ15600	AAL15957	ABS56454	AAV52223	AAA05514	ABX08179	AAT58840	AAA70149	AAH48024	ABZ16713	AAH87656	AAA38935	AAX89866	AAX89865	ABV29017	ABV23177	ABQ56733	AAH13798	AAS76802	AAD40084	AAS76803
prostate		prostate	Human prostate exp	Rabbit growth horm	DNA encoding rabbi	S. epidermidis gen	Human gene express	C. elegans CED-6 p	Human transporter	Bacillus KSM-P358	Bacillus KSM-P358	Human secreted pro	Buchnera sp. genom	Nucleotide sequenc	Streptococcus poly	Arabidopsis thalia	Human breast cance	Streptococcus pneu	Streptococcus pneu	Streptococcus pneu	S. pneumoniae type	Mycoplasma genital	Plasmodium falcipa	Internal control B	Arabidopsis thalia	Peppermint plant o	Tomato germacrene	L. esculentum germ	L. esculentum germ		Human prostate exp	Human colon cancer	Human cDNA sequenc	DNA encoding novel	Human IRAK4 short	DNA encoding novel

### ALIGNMENTS

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RESULT 1
AAD40074
Human; death domain; DD; death effector domain; DED; Chlamydia infection; MB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis; inflammation; allergy; autoimmunity; allograft rejection; cell division; immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy; gene; ss.
                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                          AAD40074 standard; cDNA; 294 BP.
                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                 Human IRAK4 DD (death domain) cDNA.
                                                         WO200240680-A2.
                                                                                                                                                                                                                                                                                         22-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                   AAD40074;
                                                                                                                                         Location/Qualifiers
                                                                                          product= "Human IRAK4 DD"
note= "No start and stop codon"
                                                                                                                   *tag= a
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chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and FPA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specifically reactive with CTDD DD fC ctrachomatis, C. muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the CTDD DD protein is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for treating bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense therapy and gene therapy. The present sequence is human IRAKA DD cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or NIDD (NGFR interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent, by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or the process of the control of the domain and the candidate binding agent, and the candidate binding agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases
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29-JUN-2001; 2001US-301889P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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DB; AAE24854.
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                                   ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC
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                                                                                                                         GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG
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                                                                                                                                                                                                                                                                                                                                                                     294 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 294; DB 24
Pred. No. 1.6e-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Matches
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                                                                                                                                                                                                                                                                        AAA09310-20 are novel genes isolated by SEREX screening from a renal cancer cell line 1973/10.4. The genes encode cancer associated antigen precursors. These gene products are useful in methods for preventing, diagnosing and/or treating disorders, especially cancer, associated with abnormal expression of human cancer associated antigens. The method comprises contacting a sample from a subject with an agent that specifically binds to the nucleic acid molecule or expression product (or fragment) complexed with a human leukocyte antigen (HLA) molecule and determining the interaction between the agent and the nucleic acid molecule or the expression product as a determination of the disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Preventing, diagnosing and/or treating disorders associated with abnormal expression of human cancer associated antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Obata Y, Go
Stockert E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-1999;
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                                                                                                                                                                                                                                                      Sequence 833 BP; 273 A; 155 C; 179 G; 226 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                 134
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                                                                                                                        1 ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
                                                                                                                                                                                                                  Similarity
                      GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG
GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG
                                                                        AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
                                                                                                 88
                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer associated antigen precursor; diagnosis;
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98US-0166350
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Y, Old LJ,
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Jager E,
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Pred. No. 2.2e-77;
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Knuth A;
                                                                                                                                                                                                                             DB 21;
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313
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RESULT 3
ADA04079
ID ADA4
XX A
The invention relates to an isolated polypeptide comprising a death C domain (DD), death effector domain (DD) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC C domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or CC (NIDD (NGFR-interacting Death Domain), with a candidate binding agent and CC detecting the association of the domain and the candidate binding agent and CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or CC chemical crosslinking, nuclear magnetic resonance (NMR), mass CC spectroscopy (MS) and FPA. The invention is useful for modulating the CC level of a cell process such as cell proliferation, cell adhesion, cell immunoglobulin class switching, in particular apoptosis within a cell. CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the CC TDD DD protein is useful for modulating the activity of oncogenic proteins, CC invention is useful for modulating the activity of bacterial for creating bacterial infections by modulating the activity of bacterial constraints and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 19; Page 180-182; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stenner-liewen F;
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29-JUN-2001;
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DB; AAE24859.
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2001US-301889P.
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RESULT 4
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ID AAS7
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DE DNA
XX Huma
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                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human;
food su
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                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                              WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                          Drmanac RT,
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                                                                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2001.
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supplement; medical imaging; diagnostic; genetic disorder;
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2000US-0649167.
                                                                        IJ
                                                                                                                                                                                                                                                                                                                          Liu C,
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                                                                        No 12609;
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Pred. No. 2.6e-77;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,

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RESULT 5
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Best Local S
Matches 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; death domain; DD; death errector versity, external infection; sepsis MB-ARC domain; apoptosis; oncogenic protein; bacterial infection; cell division; inflammation; allergy; autoimmunity; allograft rejection; cell division; inmune-based pathology; fibrosis; arthritis; graft versus host disease; immune-based pathology; fibrosis; arthritis; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein response to useful for treating disorders involving aberrant protein response have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and the protein response of data and products dependent on the and and and and and and and and are application of the protein and products are application of mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           death domain; DD; death effector domain; DED; Chlamydia infection;
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Pred. No. 2.8e-77;
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Query Match
Best Local Similarity
Matches 294; Conserv

Conservative

100.0%; Score 294; DB 24; 100.0%; Pred. No. 3.3e-77; ive 0; Mismatches 0;

Sequence 2817 BP;

912 A; 547 C; 586 G;

772 T; 0

other;

Length Indels

2817;

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Gaps

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ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC

GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG GAATTACTGTTTIGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG <u>AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT</u> AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT

> 240 253

313

밁 Ś В S

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CC is useful for identifying a binding agent, preferably a protein or a drug chart binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or NIDD (NGFR-Interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent. CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or CC chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and FPA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and cell. CC level of a protein class switching, in particular apoptosis within a cell municatum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the CTDD DD protein is useful for modulating the activity of oncogenic proteins, cc invention is useful for modulating the activity of bacterial proteins and for treating a pathology caused by the oncogenic proteins and for proteins. The protein and antibody specific for it are useful for treating immune-based pathologies, pathologies associated critical acid entropies infection, and other diseases. The protein cut is useful for treating immune-based pathologies, pathologies associated critical critical critical contents and contents associated critical critica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reed JC, Godzi
Stenner-liewen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB_ARC domain. The inven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 19; Page 194-196; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2000; 2000US-0715893
29-JUN-2001; 2001US-301889P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-NOV-2001; 2001WO-US44844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BURN-) BURNHAM INST
                                                                                cell division, inflammatory diseases such as sepsis, fibrosis, ritis, graft versus host disease. The invention is used in antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-500222/53.
DB; AAE24865.
                                                        and
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iewen F;
                                                     gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pawlowski K,
                                                        The
                                                     present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fiorentino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SH,
                                                        IRAK4 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention
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cc associated kinase (IRAK)-4. IRAK associate with activated IL-1, IL-18
CC and other receptors and act to transduce signals originating from the
CC activated receptors, ultimately leading to a variety of downstream
CC effects such as nuclear factor (NF)-kappaB activation. The IRAK-4
CC inhibitors are useful for treating inflammatory diseases such as
CC pulmonary diseases and diseases of the airway (e.g., adult respiratory
CC disease syndrome (ARDS), chronic obstructive pulmonary disease (OPD),
CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough
CC or allergic rhinitis, systemic lupus erythematosus, multiple sclerosis
CC or diabetes), cancer (e.g., solid tumours, skin cancer or lymphomal,
CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases
CC of the central nervous system (e.g., neurodegenerative disease), CD14
CC mediated sepsis, non-CD14 mediated sepsis, osteoarthritis, osteoporosis,
CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and
CC ulcerative colitis), Behcet's syndrome, ankylosing spondylitis, gout,
CC cracks colitis), Behcet's syndrome, ankylosing spondylitis, gout,
CC cracks activity or expression are used to inhibit signal transduction
                RESULT 6
AAD10197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermativis; inflammatory bowel disease; gout; Crohn's disease; ulcerative colltis; Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor; sarcoidosis; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating asthma, allergic rhinitis, multiple sclerosis and skin cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Fig 2; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JAN-2000; 2000US-0176395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JAN-2001; 2001WO-US01171.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD10197 standard; cDNA; 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibacterial; antiinflammatory; ophthalmological; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-451860/48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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RESULT 7

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21-JUN-2000; 2000US-213361P.
01-SEP-2000; 2000US-229763P.
05-SEP-2000; 2000US-230629P.
14-SEP-2000; 2000US-232658P.
19-DEC-2000; 2000US-232658P.
19-DEC-2000; 2000US-25037P.
08-JAN-2001; 2001US-260796P.
  Lung tumour polynucleotide and diagnosis of cancer especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resulting from the activation of an interleukin-1 receptor (IL-IR)/Toll receptor in a cell. They also inhibit the activation of a transcription factor that activates NFkappaB in the cell. IRAK-4 is used to create a nonhuman transgenic animal which is useful for testing the function of IRAK-4 in vivo, to generate models for the study of inflammatory disorders and conditions and for the development of potential treatments for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequences
                                                                                   WPI; 2002-010896/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-2001; 2001WO-US11859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200177168-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lung small cell carcinoma antigen, cDNA #149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS61608 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                    Wang
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Pred. No. 7.8
polypeptides useful lung cancer -
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RESULT 8
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Best Local Similarity
                                                             Mouse; interleukin-1 receptor associated kinase-4; IRAK-4; cytostatic; III, antibacterial; antiinflammatory; ophthalmological; vasotropic; OPD; chronic obstructive pulmonary disease; neuroprotective; chronic cough; adult respiratory disease syndrome; pulmonary fibrosis; asthma; ARDS; interstitial lung disease; allergic rhinitis; transplant rejection; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes; cancer; solid tumour; lymphoma; stroke; cardiovascular disease; atherosclerosis; neurodegenerative disease; sepsis; osteoarthritis; rash; osteoporosis; psoriasis; dermatitis; inflammatory bowel disease; gout; Crohn's disease; ulcerative colitis; Behcet's syndrome; ankylosing spondylitis; IL-1 receptor/Toll receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from the patient is contacted with (III), detecting the amount of polynucleotide hybridised to (III) in the sample and comparing the amount of polynucleotide to a predetermined cut-off value and thereby determining cancer in a patient. (I), (II) or antigen-presenting cells expressing (II) is useful for stimulating and/or expanding T cells specific for a tumour protein. The method comprises contacting T cells with one of the components under conditions to permit the stimulation and/or expansion of the cells. A composition comprising (I) is useful for stimulating an immune response in a patient and for inhibiting the development of a cancer especially lung cancer in a patient. An isolated T cell population is useful for removing tumour cells from the biological sample and for inhibiting the development of cancer in a patient. Assislation. Assislation is useful for removing tumour cells from the patient. Assislation. Assislation is useful for inhibiting the development of cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel isolated lung small cell cancer polynucleotides (I) and polypeptides (II) used in a method of d cancer in a patient. The method is optionally performed by utilising oligonucleotides (III), where the biological sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 174; 295pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD10198 standard; cDNA; 1542 BP
                                                                                                                                                                                                                                                                                                                                     Mouse interleukin-1 (IL-1) receptor-associated kinase (IRAK)-4
                                                                                                                                                                                                                                                                                                                                                                                 24-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer antigen coding sequences of the invention.
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                                               transgenic
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97.3%;
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                                               animal; ss
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Pred. No. 6.9e
0; Mismatches
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Best Loc Matches Query Match

238;

Conservative

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Mismatches

Indels

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Length 1542;

Local

Similarity

69.5%;

Score 204.4; Pred. No. 1.

.1e-50; В 56; 22; Sequence 1542 BP;

421 A;

392

C; 423

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306 T; 0 other;

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AATCAGTITCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT CAAGAAGGGTGGAAGAATTAGCAGTAGCTATCAAAAAGCCCGTCCGGCGACGACAGATAC ACATACATACGCAACCTTAATGTGGGGATCCTTAGGAAGCTGTCGGATTTTATTGATCCT ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT

180 306 120 246 60

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CC disease syndrome (ARBS), chronic obstructive pulmonary disease (ODD), CC pulmonary fibrosis, interstitial lung disease, asthma, chronic cough CC or allergic rhinitis), transplant rejection, autoimmune diseases (e.g., crheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis CC or diabetes), cancer (e.g., solid tumours, skin cancer or lymphoma), CC cardiovascular diseases (e.g., stroke and atherosclerosis), diseases (e.g., stroke and atherosclerosis), diseases of the central nervous system (e.g., neurodegenerative disease), CD14 CC mediated sepsis, onsteoarthritis, osteoporosis, CC psoriasis, diseases of the skin (e.g., rash, contact dermatitis, atopic CC dermatitis), inflammatory bowel disease (e.g., Crohn's disease and CC culcarative colitis), Behcet's syndrome, ankylosing spondylitis, gout, CC sarcoidosis and ophthalmic diseases and conditions. The inhibitors of CC RAK-4 activity or expression are used to inhibit signal transduction CC receptor in a cell. They also inhibit the activation of a transcription canoniuman transgenic animal which is useful for testing the function of CC RAK-4 in vivo. to cenerate models for the strind of inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a cDNA encoding mouse interleukin (IL)-1 recept associated kinase (IRAK)-4. IRAK associate with activated IL-1, IL-18 and other receptors and act to transduce signals originating from the activated receptors, ultimately leading to a variety of downstream effects such as nuclear factor (NF)-kappaB activation. The IRAK-4 inhibitors are useful for treating inflammatory diseases such as pulmonary diseases and diseases of the airway (e.g., adult respiratory diseases and diseases of the airway (e.g., adult respiratory diseases).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human interleukin-1 receptor associated kinase polypeptide, useful for identifying modulators of the polypeptide for treating asthma, allergic rhinitis, multiple sclerosis and skin cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                             IRAK-4 in vivo, to generate models for the study of inflammatory disorders and conditions and for the development of potential treatments for IRAK-4-related inflammatory diseases and conditions. IRAK-4 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUL-2001.
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                                            are also used in
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1..1542
/*tag= a
/product= "Mouse IRAK-4"
                                         gene therapy and in antisense therapy.
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                                             polynucleotides are also used in diagnostics as expressed sequence tags of or identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and camino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences, (PCR) primers, oligomers, and for chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                           polypeptide (II) sequences. (I) is useful as hybridisation proplymerase chain reaction (PCR) primers, oligomers, and for and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000;
23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #12607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      supplement;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID No 12607; 103pp; English.
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2000US-0649167.
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medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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Query Match

Sequence

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Score 150.4; Ģ. 142 H .. 0 DВ other; 23;

Length 405;

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RESULT 10
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The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or NIDD (NGFR-interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent, by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and FPA. The invention is useful for modulating the
                                                                                                                                                                                                            New polypeptide comprising a death domain or death effector domain, useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases
                                                                                                                                                                    Claim 19;
                                                                                                                                                                                                                                                                                                                       Stenner-liewen
                                                                                                                                                                                                                                                                                                                                     Reed JC,
                                                                                                                                                                                                                                                                                                                                                                                                29-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200240680-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune-based pathology; fibrosis; arthritis; graft versus host disease; immunosuppressive; gene therapy; antisense therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human IRAK4 short gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD40084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD40084 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'unman; death domain; DD; death effector domain; DED; Chlamydia inf
'NB-ARC domain; apoptosis; oncogenic protein; bacterial infection;
inflammation; allergy; autoimmunity; allograft rejection; cell div.
mmune-based pathology; fibrosis; arthritis; graft versus host die
                                                                                                                                                                                                                                                                         2002-500222/53.
DB; AAE24864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 TAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCTGAATTACTGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151; Conservative
                                                                                                                                                                                                                                                                                                                                                                   BURNHAM INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTGATCCAAAATGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCTGAATTACTGTTTG
                                                                                                                                                                                                                                                                                                                       Godzik A, iewen F;
                                                                                                                                                                   Page 195; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                2000US-0715893.
2001US-301889P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Human IRAK4 short protein"
                                                                                                                                                                                                                                                                                                                                     Pawlowski
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                                                                                                                                                                                                                                                                                                                                   ~
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                                                                                                                                                                                                                                                                                                                                   Fiorentino
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                                                                                                                                                                                                                                                                                                                                   Lee
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RESULT 11
AAS76802
ID AAS76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        level of a cell process such as cell proliferation, cell adhesion, cell cursus responses, responses to microbial infection and B cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specifically reactive with CTDD DD of C. trachomatis, C. muridarum, C. pneumoniae, and C. psitraci or a nucleic acid encoding the CTDD DD protein is useful for modulating a Chlamydia infection. The convention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for treating bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense of the protein content of the protein of the protein and content of the protein antisense.
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Best Local S
Matches 140
                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS76802 standard; cDNA; 415
                                                                                                                                  P-PSDB;
                                                                                                                                                                                         Drmanac
                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                            11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                     WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy and gene therapy. The present sequence is human IRAK4 short gene
                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                    2001-639362/73
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                                                                                                                                                                                       RT,
                                                                                                                                  ABG12615.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATCAGTTTCACATAAGGAGATTT 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 BP; 77 A; 41 C; 36 G;
                                                                                                                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human diagnostic protein #12606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
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                                                                           mutations
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Claim 1; SEQ ID No 12606; 103pp; English

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RESULT 12
AAA113
AXX AAA13
AXC AAA13
AXC AAA13
AXC AAA13
AXC AAA13
AXC Human
XX Human
XX Human
XX Homo
OS Homo
OS Homo
OS Homo
VX EP107
XX 29-JU
PF 28-JU
PF 27-AU
PR 27-AU
PR 11-JA
PR 02-JU
PR 11-JA
PR 09-JU
XX Ota T
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XX Ota T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynuclectide (I) and CC polymerase (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags CC polynuclectides are also used in diagnostics as expressed sequence tags CC (II). (II) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polymeptide and polynuclectide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention. CC diagnostic coding sequences of this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at figure the invention of the printed specification, but was obtained in electronic format directly from WIPO at figure the invention of the printed specification.
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Best Local (
                 Ota T, Ishii S,
                                                                                                                                                                                                                                                                                                                                                                        Human cDNA sequence SEQ ID NO:10742.
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH13798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH13798 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 415 BP; 144 A; 83 C; 78 G;
                                                                                                                   11-JAN-2000;
02-MAY-2000;
                                                                                                                                                    29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                      28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                       07-FEB-2001.
                                                                                                                                                                                                                                                                       EP1074617-A2
                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                     Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                         26-JUN-2001
                                                                   (HELI-) HELIX RES
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               Isogai T,
, Sugiyama
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                                                                                                   ; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                    99JP-0248036.
99JP-0300253.
                                                                                                                                                                                                                                                                                                                                     detection; diagnosis; antisense therapy; gene therapy; ss.
               Nishikawa T,
T, Wakamata
                                                                   INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.8%;
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                   Wakamatsu
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                 Hayashi K,
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144
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                   Saito K,
K, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.
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                    Yamamoto
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RESULT 13
ABQ56733
ID ABQ56
XX ABQ56
XX ABQ56
XX ABQ56
XX Humar
XX Humar
XX Humar
XX Humar
XX Homo
XX Homo
QX Homo
QX Homo
QX Homo
QX Homo
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                           genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                   02-AUG-2002
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  02-OCT-2000; 2000US-237271P
                                                           02-OCT-2001; 2001WO-US30732.
                                                                                                                   11-APR-2002
                                                                                                                                                                                                                                                                                                                                                                        Human colon cancer related nucleotide sequence SEQ ID NO:428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                           WO200229086-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABQ56733 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _
                                                                                                                                                                                                                                                                                                                colon cancer; cancer; tissue profiling;
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                                                                                                                                                                                                                                                                                        analysis;
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                                                                                                                                                                                                                                                                                        diagnostic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.8%;
97.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 137.6;
Pred. No. 8.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                     antisense therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           918
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                                                                                                                                                                                                                                                                                                                forensic; mapping;
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                                                                                                                                                                                                                                                                                     gene;
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Matches Query Match

Local

Similarity

35.6%;

Conservative

0, Pred. Score 104.8;

Mismatches No.

Indels Length

Gaps

BB 24;

408; 10;

Sequence 408 BP; 114 A; 92 C; 81 G; 61 T; 60 other;

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CC expressed in cancer tissues. ABB78993 to ABB78993 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 1; 796pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or tissue type, and in antisense therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-426115/45
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ABV23177 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                           NNANAANGANGG-ANAAGGCAGCTGNAGCTATNAAAAAACCANCNGGGGATGATNNGATA
                                                                                                                                                                                                                                                                                                                                                                                 CAAGAAGGATGGAAGAAGTTAGCTGTAGCTATTAAAAAACCATCTGGTGATGAT-AGATA 119
                                                                                                                                                                                                                  CTTCTGAAT-TACTGTTTGACTGGGGCACCACAAATTGCACAGTT-GGTGATCTTGTGGA
                                                                                                                                                                                                                                                            CCATCAGTTTCACANANNGGAGATNTGAAGCATTACTNNAAAACTGGGAAAAAAGGCCCN
                                                                                                                                                                                                                                                                                                 CAATCAGTTTCACATA-AGGAGATTTGAAGCATTACTTCAAA---CTGGAAAAAGTCCCA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACATATGTGCGCTGCATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 60
                                                                                                  TNCCNCGAANCACAACNGAATTTNTNGCTCCNTGCNANGCCNGGGCNCCCAGACGCNG
                                                                                                                                     TCTTTTGATCCAAAATGAATTTTTTG--CTCCTGCGAGTCTTTTGCTCCCAGATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                          ACNTGTCGGNCCCTGCCNNATGGTGGNCTAATNANGAAGCNGNCAGANTTTANCGANCCT
2378
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81;
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RESULT 14
ABV23177
ID ABV23
XX
AC ABV23
XX
DT 16-SE
DT 16-SE
XX
WHUMAI
XX
HUMAI
XW Pharm
XX
OS Homo
XX
                                                     Human prostate
                                                                        16-SEP-2002
                                                                                         ABV23177;
                                                                      (first entry
                                                     expression marker cDNA 23168
                         cytostatic;
gene; ss.
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Homo sapiens pharmacogenomic

prostate

cancer;

carcinogen;

pharmacodyanamic marker;

WO200160860-A2

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RESULT 15
ABV29017
ID ABV29
XX
AC ABV29
XX
DT 16-SE
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Best Local
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(d) assessing

in a patient;

(e) selecting

(f) assessing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of t specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usef for detecting presence of prostate cancer, stage of prostate cancer
    Human
                             16-SEP-2002
                                                                               ABV29017
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schlegel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastazed in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                ient ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cer in a patient, assessing the ef
                                                                                                                                                                                                                                                                                                      467
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  prostate
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                                                                               standard;
                                                                                                                                             AGGTAGTGATTGAAACTGGGGCTGTTCCGATTTTTAT
                                                                                                                                                                                               TACAATTTGAAGCTGCATGGGCATTAACAAATATAGCATCTGGAACTTTTCTGCATACCA
                                                                                                                                                                                                                          CTGAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTT
                                                                                                                                                                                                                                                                            ACAATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTT
                                                                                                                                                                                                                                                                                                     CACAGAAATTTAGAAAGCTGCTTTCTAAAGAACCTAATCCACCAATAGATCAAGTTATAC
                                                                                                                                                                                                                                                                                                                               CTCAAGAAGGATGGAAGAAGTTAGCTGTAGCTATTAAAAAACCATCTGGTGATGATAGAT
                                                                                                                                                                       TGATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTT
                                                                                                                                                                                                                                                   AGAAACCAGGAGTTGTACAGAGATTTGTGAAATTTCTTGAAAAGAAATGAAAATTGCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                  useful
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2000US-211314P.
2000US-219007P.
2000US-255281P.
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2000US-189862P.
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                                                                                                                                                                                                                                                                                                                                                                                                         B₽;
  expression marker cDNA 29008
                                                                                                                                                                                                                                                                                                                                                                                                          769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         efficacy of a therapy for inhibiting
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                                                                               cDNA;
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                                                                               2378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolated nucleic acid molecule (I in Tables 1-9 (ABV00010-ABV62213)
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                                                                                                                                                                                                                                                                                                                                                       Score 42.6; D
Pred. No. 0.01
0; Mismatches
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0.015;
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                                                                                                                                                                                                                                                                                                                                                       Gaps
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Best
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25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of a specification or its complement, (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer in a patient;
(d) assessing the efficacy of a therapy in a patient;
(e) selecting a composition for inhibiti (f) assessing the prostate cell carcinog (g) determining whether prostate cancer (h) assessing the aggressiveness or indo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2378 BP; 769 A; 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schlegel
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13-DEC-2000;
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                                                                            587
647
                                                                                                                                                                                                119
                                                                                                                                                                                                                                       467
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                                                                                                                                                                                                                                                                              59
                                                                                                                                                                                                                                                                                                                                                                                                                                       also useful
                                                                                                                                                                                                                                                                                                                                          Similarity
                                     TGATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTT
                                                                            TACAATTTGAAGCTGCATGGGCATTAACAAATATAGCATCTGGAACTTTTCTGCATACCA
                                                                                                                 CTGAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGGATCTTTT
                                                                                                                                                                                           ACAATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTT
                                                                                                                                                                                                                                       CACAGAAATTTAGAAAGCTGCTTTCTAAAGAACCTAATCCACCAATAGATCAAGTTATAC
                                                                                                                                                                                                                                                                        CTCAAGAAGGATGGAAGAAGTTAGCTGTAGCTATTAAAAAACCATCTGGTGATGATAGAT
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                                                                                                                                                          Conservative
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2000US-207454P.
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gene; ss.
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                     Mismatches
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10B_PUB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10B_PUB.seq:*

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18: /cgn2_6/ptodata/1/pubpna/US10B_PUB.seq:*
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294
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

15	14	13	12	11	10	9	8	7	δ	v	4	ω	N	1	Result No.
33.8	33.8	36	40.4	40.4	40.4	137.6	151.8	204.4	241.6	292.4	294	294	294	294	Score
11.5	11.5	12.2	13.7	13.7	13.7	46.8	51.6	69.5	82.2	99.5	100.0	100.0	100.0	100.0	Query Match
22684	22684	2000	2024	2024	2024	211	31000	1542	501	1383	2817	2817	1383	294	Query Match Length
13	13	10	11	ø	9	15	11	H	9	11	15	11	15	15	DB
US-09-960-870-2	US-09-960-858-2	US-09-938-842A-4518	US-09-900-797-51	US-09-903-012-51	US-09-887-586A-51	US-10-001-254-25	US-09-966-451-10	US-09-759-595-4	US-09-833-790-149	US-09-759-595-2	US-10-001-254-27	US-09-966-451-3	US-10-001-254-15	US-10-001-254-5	ID
Sequence 2, Appli	Sequence 2, Appli	Sequence 4518, Ap	Sequence 51, Appl	Sequence 51, Appl	Sequence 51, Appl	Sequence 25, Appl	Sequence 10, Appl	Sequence 4, Appli	Sequence 149, App	Sequence 2, Appli	Sequence 27, Appl	Sequence 3, Appli		Sequence 5, Appli	Description

45	C 44	43	42	41	40	39	38		c 36		34	33	32		c 30				26	25			c 22		20	19	18	c 17	
31.8	32	32	32	32	32		32.2	32.2	32.2	Ŋ	32.2	32.2	32.6	N	32.8	N	N	ω u	33	33	<b>3</b> 3	ω L	33	33	33.2	33.2	33.2	33.6	33.8
10.8	10.9	10.9	10.9	10.9	10.9	11.0 3	11.0	11.0	11.0	11.0	11.0	11.0	11.1	11.2 2	11.2 2	11.2	11.2	11.2 6	11.2	11.2	11.2	11.2	11.2	11.2	11.3	11.3	11.3	11.4	11.5 5
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US-09-918-995-3050	US-08-781-986A-37	US-09-919-039-167	US-09-880-107-3412	US-10-102-524-227	US-09-878-574-15709	US-10-312-841-2	US-10-198-846-9909	US-09-938-842A-4674	US-10-027-632-121917	US-10-027-632-121917	US-10-027-632-282173	US-10-027-632-282173	US-10-101-510-42	US-10-274-990-3	US-09-734-674-3	US-10-027-632-291958	US-10-027-632-291958	US-09-790-988-1	US-10-292-798-637	US-10-017-161-727	US-10-027-632-110061	US-10-027-632-110060	US-10-027-632-110061	US-10-027-632-110060	US-09-887-576-288	US-09-938-842A-3405	US-10-198-846-7068	US-09-769-787-287	US-10-205-220-1
Sequence 3050, Ap	Sequence 37, Appl			Sequence 227, App	Sequence 15709, A	Sequence 2, Appli		Sequence 4674, Ap		Sequence 121917,	Sequence 282173,		Sequence 42, Appl	Sequence 3, Appli	Sequence 3, Appli				637,	Sequence 727, App	Sequence 110061,		Sequence 110061,		288,	3405		Sequence 287, App	Sequence 1, Appli

### ALIGNMENTS

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US-10-001-254-5
                                                                       Query Match
Best Local Simi
Matches 294;
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Publication No. US20030049702A1
                                                                                                                                                                                                                                                               SEQ ID NO 5
LENGTH: 294
                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(294)
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Stenner-Liewen, Frank
TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins
FILE REFERENCE: P-LJ 5037
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                     h 100.0%; Score 294; DB 15; Similarity 100.0%; Pred. No. 6.4e-75; 94; Conservative 0; Mismatches 0;
                                 ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee, Sug Hyung
Roth, Wilfred
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                                                                                                        Length 294;
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60
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0

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SEQ ID NO 15
LENGTH: 1383
TYPE: DNA
TYPE: DNA
CRCANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1380)
US-10-001-254-15
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APPLICANT: Reed, JC
APPLICANT: Godzik,
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Best Local Similarity
Matches 294; Conserv
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CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
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APPLICANT: Stenner-Liewen, Frank
TITLE OF INVENTION: No. US20030049702Alel Death Domain Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSEQ for Windows Version
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PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
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   241
                                   205
                                                     181 GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG
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                                                                                                                                 121 AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
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                                                                                                                                                                                      ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTTGCTCCCAGATGCTGTTCCC
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                                                                                                   AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
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Roth, Wilfred
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Pawlowski, Krzysztof
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                                                                                                                                                                                                                                                                                                100.0%; Score 294; DB 15;
100.0%; Pred. No. 1.3e-74;
ative 0; Mismatches 0;
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US-09-966-451-3
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US-10-001-254-27
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                 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 88
SEQ ID NO 3
LENGTH: 2817
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     Sequence 27, Application US/100 Publication No. US20030049702A1
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Best Local Similarity
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APPLICANT:
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APPLICANT: Susan M. Freier
IITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
FILE REFERENCE: RTS-0324
CURRENT APPLICATION NUMBER: US/09/966,451
CURRENT FILING DATE: 2001-09-28
                                                                APPLICANT: Stenner-Liewen, Frank
TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins
FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                              APPLICANT: Reed, John C. APPLICANT: Godzik, Adam
                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
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LOCATION: (50)...(1432)
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LENGTH: 2817
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Roth, Wilfred
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Fiorentino, Loredana
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                                       for Windows Version
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100.0%; Pred. No. 1.9e-74;
tive 0; Mismatches 0;
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ORGANISM: Homo sapien

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GENERAL INFORMATION:

APPLICANT: Wesche, Holger

APPLICANT: Li, Shyun

APPLICANT: Li, Shyun

APPLICANT: Thiarik Inc.

TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use

FILE REFERENCE: 018791-003910US

CURRENT APPLICATION UMMBER: US/09/759,595

CURRENT FILING DATE: 2001-01-13

PRIOR APPLICATION NUMBER: US 60/176,395

PRIOR FILING DATE: 2000-01-13

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2
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                                                                                                                                                                                                                                           ; LOCATION: (1)..(1383)
; OTHER INFORMATION: human IRAK-4
US-09-759-595-2
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US-09-759-595-2
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; NAME/KEY: CDS
; LOCATION: (50)...(1429)
US-10-001-254-27
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Best Local Similarity
Matches 293; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                  CAAGAAGGATGGAAGATTAGCTGTÄGCTATTÄAAAAAACCATCTGGTGATGATÄGATÄC 144
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ilarity .99.7%;
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                                                                                                                                                                           Score 292.4; DB 1
Pred. No. 3.9e-74;
0; Mismatches 1
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Pred. No. 1.9e-74;
Nismatches 0;
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RESULT 7
US-09-759-595-4
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APPLICANT: Indirias, Carol Y.
APPLICANT: Fan, Liqui
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THITILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-833-790-149
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Sequence 4, Application US/09759595 Publication No. US20030059916A1 GENERAL INFORMATION:
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LOCATION: (1)...(501)
OTHER INFORMATION: n = A,T,C
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ORGANISM: Homo sapien
FEATURE:
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97.3%;
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Pred. No. 1.1e-59;
0; Mismatches 4
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APPLICANT: Wesche, Holger
APPLICANT: Li, Shyun
APPLICANT: Tularik Inc.
APPLICANT: Tularik Inc.
TITLE OF INVENTION: IRAK-4: Compositions and Methods of Use

FILE REFERENCE: 018781-003910US

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; OTHER INFORMATION: murine IRAK-4
US-09-759-595-4
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                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                          SEQ ID NO 10
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Best Local Similarity
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                                                                                                               Matches 156;
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CURRENT FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 60/176,395
PRIOR FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                              APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freter
TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-4 EXPRESS
FILE REFERENCE: RTS-0324
CURRENT APPLICATION NUMBER: US/09/966,451
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: murine IL-1 receptor-associated kinase 4 (IRAK-4) OTHER INFORMATION: cDNA
                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus sp.
                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                         LENGTH: 31000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 1542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 ACATACATACGCAACCTTAATGTGGGGATCCTTAGGAAGCTGTCGGATTTTATTGATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238;
     183 ATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTGAT
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                                                           TCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAACTGCTGTTTGACTGGGGCACCACGAACTGCACAGTTGGCGACCTTGTGGATCTACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATCAGTTCCATATAAGGAGATTCGAAGCCTTACTTCAGACCGGGAAGAGCCCCCACCTGT
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                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.5%;
                                                                                                                              51.6%;
95.7%;
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                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 204.4; DB 1
Pred. No. 1.1e-48;
0; Mismatches 56
                                                                                                                              Score 151.8; DB : Pred. No. 7.4e-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
                                                                                                                                               DB 11; Length 31000;
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                                                                                                             Indels
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                                        13012
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Sequence 51, Application US/09887586A
Patent No. US2002094556A1
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. US20020094556A11, Jose;
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
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; NAME/KEY: CDS
; LOCATION: (1)...(177)
US-10-001-254-25
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US-10-001-254-25
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                                                                                                                                                                                                                                                                                                                        RESULT 10
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LENGTH: 211
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TITLE OF INVENTION: No. US20030049702A1el Death Domain
FILE REFERENCE: P-LJ 5037
CURRENT APPLICATION NUMBER: US/10/001,254
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR PHILING DATE: 2001-11-17
PRIOR PHILING DATE: 2001-06-39
PRIOR PHILING DATE: 2001-06-39
PRIOR FILING DATE: 2001-06-39
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PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
                                                                          FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/887,586A
CURRENT FILING DATE: 2001-06-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 46.8%;
Local Similarity 97.2%;
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                                                                                                                                                                                                                                                                                                                                                                                      145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATCAGTTTCACATAAGATGCTGT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACATATGTGCGCTGCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
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Pred. No. 8.5e-30;
0; Mismatches 4;
                                                                                                                                                                                                   Joseph
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US-09-903-012-51
                                                                                                         ; OTHER INFORMATION: VFNT germacrene C synthase US-09-903-012-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 51, Application UPatent No. US20020094557A1
GENERAL INFORMATION:
                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 58
SOFTWARE: FRASTSEQ for Windows Version
SEQ ID NO 51
LENGTH: 2024
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LENGTH: 2024
TYPE: DNA
ORGANISM: Lycopersicon esculentum
                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/903,012
CURRENT FILING DATE: 2001-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chappell, Joseph APPLICANT: No. US200200945
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: SYNTHASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR FILING DATE: 1999-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                        TYPE: DNA ORGANISM: Lycopersicon esculentum
                                                                                                                                           NAME/KEY: CDS
LOCATION: (32).
                                                                                                                                                                                 FEATURE:
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LOCATION: (32)...(1
OTHER INFORMATION:
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45 AGATTTTATTGATCCTCAAGAAGGATGGAAGAAGTTAGCTGTAGCTATTAAAAAACCATC 104
                                   98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTTGTGGATCTTT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Starks, Courtney M.
Manna, Kathleen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCAAGAGACAGGTTGGTTGAGTGTTACTTCTGGATATTAGGAGTGTATTTTGAGCCAAA 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTGATGATAGATACAATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAGCTTAGTGATCTTACAAGGTGGTGGAAAGATTTGGATTTTGCAAATAATATCCATA 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATATAGTCGTGCGAGAAAAATGATGACAAAAGTACTCAACCTGACCTCCATTATTGACGA 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No. US20020094557A11,
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                                   Conservative
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N: VFNT
                                                                                                                                             . (1675)
                                               13.7%;
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                                Score 40.4; DB 9; Pred. No. 0.31; 0; Mismatches 96
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                                                                   Length 2024;
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RESULT 13
US-09-938-842A-4518
US-09-938-842A-4518
; Sequence 4518, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
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US-09-900-797-51
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Publication No.
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CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US/09/398,395
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chappell, Joseph
APPLICANT: No. US20030087406A11,
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/130,628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (32)...(1675)
OTHER INFORMATION: VFNT germacrene C synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
TYPE: DNA
ORGANISM: Lycopersicon esculentum
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                     874
                                                                                                                                              934 CACTTTTGATGCTT
                                                                                                                                                                                                                                                        165 AAAAAGTCCCACTTCTGAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGA 224
                                                                                                                                                                                                                                                                                                                             105 TGGTGATGATAGATACAATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGG 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                           98;
                                                                                                                                                                                                                     ATATAGTCGTGCGAGAAAAATGATGACAAAAGTACTCAACCTGACCTCCATTATTGACGA
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50.5%;
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US-09-960-858-2
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; TYPE: DNA
; ORGANISM: M. genitalium
US-09-960-858-2
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CURRENT APPLICATION NUMBER: US/09/960,858
CURRENT FILING DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 19
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NANOMACHINE COMPOSITIONS AND METHODS OF TITLE OF INVENTION: USE
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TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
17674 CTAACAGTCTTAT 17686
                                                                       17614 TTAATCGCTACTCAATTACTCCTATAGTTGATCCTGAAACACAAAAAAACTATTGTAGAAG 1767
                                                                                                                                                17554
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                                  CIGCGAGICITIT 275
                                                                                                                                                Conservative
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Pred. No. 5.8;
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RESULT 15 US-09-960-870-2

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; ORGANISM: M. genitalium
US-09-960-870-2
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APPLICANT: EVANS, Glen
APPLICANT: EVANS, Glen
TITLE OF INVENTION: NANOMACHINE COMPOSITIONS AND METHODS OF
TITLE OF INVENTION: USE
FILE REFERENCE: P-EA 4738
CURRENT APPLICATION NUMBER: US/09/960,870
CURRENT FILING DATE: 2001-09-20
RUMBER OF SEQ ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 22684
                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 71; Conserv
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                                                                        17614 TTAATCGCTACTCAATTACTCCTATAGTTGATCCTGAAACACAAAAAAACTATTGTAGAAG 17673
                                                                                                                                                      263 CTGCGAGTCTTTT 275
                                                                                                               203 CCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTGATCCAAAATGAATTTTTTTGCTC 262
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CTAACAGTCTTAT 17686
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Pred. No. 80;
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Search completed: January 18, 2004, 01:19:33 Job time : 218 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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1 acatatgtgcgctgcctcaa.....tgctcccagatgctgttccc 294
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

AUTHORS	SOURCE ORGANISM	RESULT 1  AX431296  LOCUS  DEFINITION  ACCESSION  VERSION  KEYWORDS		4 4 5	42 43	41	39	c 37	ა ( წ		C 33	) LJ (	2 2 0 9	28		25	2 2 3					15							ហារ	·ω	NΗ	1	Result No. S	
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ino,L., Godzik, iewen,F. oteins	Chordata; Craniat; Primates; Catarrh	294 bp WO0240680.	ALIGNMENTS	AR240709 AR266984	AF279453 AR183921	AF035630 AF279454	AR183920	CNS061K2	CNS06IST	AC008732	AF2/9456 AL139425	BC047409	BV034947	AE010646	AC134788_3	BV075713	AC123081	AC129390 BC045381	AK027301	AX431316	AC021/19 AC025567	AC093012	BC051676 AY186092	AF445803	AX321132 AX196262	BC013316	AX196260 AF445802	AK000528	AF155118	AX431306	AR223870	, ; , ; , ;	ID	SUMMARIES
A., Lee,S.H., Reed,J.C.,	ata; Vertebrata; Euteleostomi; rhini; Hominidae; Homo.	DNA linear PAT 28-JUN-2002		AR240709 Sequence AR266984 Sequence	AF279453 Lycopersi AR183921 Semience	ycopers	equence	T3 end	T7 end o	AC008732 Homo sapi	AFZ/9456 LYCOPERSI	BC047409 Homo Sapi	BV034947 S212P6037	usobacte	2 2 2 2 3 2	S212Pe	AC123081 Rattus no	ᅜ	AK027301 Homo sapi	Sequence	Ното вар	AC093012 Homo sapi	Homo sar	Mus mu	Seque	BC013316 Homo sapi	Sequence	Homo	Sequence Homo sap	Seque	AX431296 Sequence AR223870 Sequence		Description	

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                                                                                                                                                                                   Renal cancer associated antigens and Patent: US 6440663-A 10 27-AUG-2002; Location/Qualifiers
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Scanlan, M.J., Stockert, E., Chen, Y.-T.,
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                                                                                     h 100.0%;
Similarity 100.0%;
94; Conservative 0
                                                                                                                                                                                                                                                                Unclassified.
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/db_xref="G1:21656166"
/translation="TYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSGDDRYNQFH
/translation="TYVRCLNVGTINCTVGDLVDLLIQNEFFAPASLLLPDAVP"
IRRFEALLQTGKSPTSELLFDWGTTNCTVGDLVDLLIQNEFFAPASLLLPDAVP"
a 55 c 62 g 93 t
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155 c 179 g
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ol_type="genomic DNA"
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Roth,W. and Stenner-Liewen,F.
Novel death domain proteins
Patent: WO 0240680-A 15 23-MAY-2002;
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Sequence 15 from Patent WO0240680.
AX431306
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                   GAATTACTGTTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG
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/bryngfiireallotskeptsekledwrthroughurligneefapasille
DAVYNGFIIREEALLOTGKSETSELLFDWGTTNCTVGDLVDLLIGNEEFAPASILLEV
DAVFKTANTLPSKEAITVQQXQMPFCDKDRTIMTPVQNLEQSYMPDSSSPENKGLEV
SDTRFHSFSFYELKNVINNFDERPISVGGENKWGEGGFGVVYKGYVNNTTVAVKKLAAM
VDITTEELKQQFDQEIKVMAKQQHENLUELLGFSSDGDDLCLVYVYNENGSLLDRLSC
LDGTPPLSWHMRCKIAQGAANGINFLHENHHIHRDIKSANILLDEAFTAKISDFGLAR
ASEKFAQTVMTSRIVOTTAYMAPEALIGGITPKSDIYSFGVVLLEITGAFSCHERK
ASEKFAQTVMTSRIVOTTAYMAPEALIGGITPKSDIYSFGVVLLEITGAFTAKISDFGLAR
ASEKFAQTVMTSRIVOTTAYMAPEALIGGITPKSDIYSFGVVLLEITGAFTAKISDFGKKV
PQLLLDIKEEIEDEEKTIEDYIDKKMNDADSTSVEAMYSVASQCLHEKKNKRPDIKKV
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/db_xref="GI:21656176"
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/codon_start=1
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|mol_type="genomic DNA"
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Pred. No. 1.2e-64;
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Novel death domain proteins
Patent: WO 0240680-A 27 23-MAY-2002;
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Homo sapiens
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                                                                                        ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC
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DDRYNQFHIRRFEALLQTGKS PTSELLFDWGTTNCTVGDLVDLLIQNEFFAPASLLLF
DDRYNQFHIRRFEALLQTGKS PTSELLFDWGTTNCTVGDLVDLLIQNEFFAPASLLLF
BAVPKTANTLES KEAITVQQKQMPFCDKDRTLMTPVQNLEQSYMPPDSSS PENKSLEV
SDTRFHSFS FYELKNVTNNFDER PIS UGGNKMGEGGFGVVLKYLAVKKLAV
VDITTEELKQQPDQEIKVMAKCQHENLVELLGFSSDGDDLCLKYVYMMSSLLDRLSG
LDGTPPLSWHMRCKIAQGAANGINFLHENHHIHRDIKSANILLDEAFTAKISDFGLAR
ASEKFAQTVMTSRIVGTTAYMAPEALAGEITPKSDIYSFGVVLLEIITGLPAVDEHRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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DEFINITION
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Submitted (28-MAY-1999) Ludwig Institute,
Institute, 1275 York Ave, New York, NY 100
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Jongeneel, V., Gure, A.O., J
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ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 294
                                                                     GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGGATCTTTTTG
                                                                                                                                                             AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
                                                                                                                                                                                                                             AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCCACTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / traislation="MMKPITPSTYVRCLNVGLIRKLSDFIDPOEGWKKLAVAIKKPSG
DDRYNOFHIRRFEALLQTGKSPTSELLFDWGTTNCTVGDLVDLLGNEFFAPASLLLF
DAVFKTANTLESKEAITYQOKOMFFCDKDRTLMTPVQNLEGSYMPPDSSSPENKSLEV
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VDITTELSKEATYQOKOMFFCDKDRTLMTPVQNLEGSYMPDSSSPENKSLEV
VDITTELKQOFDQEIKVMAKOQHENLVELLGFSSDGDDLCLVYYNMENGSLLDRLSC
LDGTPPLSMHARCKLAQGAANGIURLHENHHIRDIKSANILLDEAFTAKISDFGLAR
ASEKFAQTVMTSRIVGTTAYMAPEALRGEITPKSDIYSFGVVLLEIITGLPAVDEHRE
PQLLLDIKEBIEDEKTIEDYIDKKWNDADSTSVEAMYSGASQCRHEKKNKSPDIKKV
HQLLOEMTAS"

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/db_xref="GI:5360131"
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Location/Qualifiers
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Pred. No. 1.1e-64;
; Mismatches 0;
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Chen, Y.-T.
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121 AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT 180	CAAGAAGGATGGAAGAAGTTAGCTGTAGCTATTAAAAAACCATCTGGTGATGATAGATA	CARGRADICIPATICATA CONTROL TRACTOR AND A CONTROL TRACTOR AND A CONTROL A	54 ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTAATGATCCT 113	1 ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 60	tch 100.0%; Score 294; DB 9; Length 2820; al Similarity 100.0%; Pred. No. 1.1e-64; 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	940 a	//HOUSE="LUIMAINED PLOCELL PLOQUECT" //COGON SEARTE-I //COGON SEARTE-I //DroteIn_id="BAA91232.1" //db xref="rGI:7020694" //db	/note="cloning vector pME18SFL3" 301412	/cell_inb="KAT"  /clone_lib="KAT"	mol_t	12820	Agency). Location/Qualifiers	sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency)	NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert	University of Tokyo, Deptment of Virology; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel.81-3-5449-5986 Fay:81-3-5449-5416)	Direct Submission Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science,	2 (bases I to 2820) Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,	Nakamura,Y., Isogai,T. and Sugano,S.  Nakamura,Y., Isogai,T. and Sugano,S.  NEDO human cDNA sequencing project  Importable bed	0,H.,	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		AK000528 (2820 bp mRNA linear PRI 22-FEB-2000) HOMO Bapiens CDNA FLJ20521 TIB, Clone KAT10395.	

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                                                                                                         145 AATCAGTITCACATAAGGAGATITGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
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241 ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 294
                                   205 GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGCTGGTGATCTTGTGGATCTTTTG
                                                                       181 GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTG
                                                                                                                                121 AATCAGTTTCACATAAGGAGTTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
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Sequence 2 from Patent W00151641.
AXI96260
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Patent: WO 0151641-A 2 19-JUL-2001;
Tularik Inc. (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DDRYNQFHIRREEALLQTGKS9TSELLFDWGTTNCTRAEDLVDLLIQUBEFARASLLLF
DAVPKTANTLPSKEAITVQQKQMFFCDXDRTHATPVQNLEQSYMPPDSSSPENKSLLV
SDTRFHSFSFYELKNVTNMFDERFISVGSNKGEGGFGVVYKGYVNNTTVSAPVKKLAAM
VDITTEELKQQFDQEIKVMAKCQHENLVELLGFSSDGDDLCLVYVYMPNGSLLDRLSC
LDGTPPLSWHMECKLAQGAANGINFLHENHHHHRDIKSANILLDEAFTAKISDFGLAR
ASEKFAQTVMTSRIVGTTAYMAPEALRGEITPKSDIYSFGVVLLEIITGLPAVDEHRE
PQLLLDIKEBIBDEEKTIEDYIDKKMNDADSTSVEAMYSVASQCLHEKKNKRPDIKKV
QQLLQEMTAS"
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/protein_id="CAC60090.1"
/db_xref="GI:15386463"
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/db_xref="taxon:9606"
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Pred. No. 3.1e-64;
0; Mismatches 1;
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Suzuki, S., Duncan, G.S., Millar, D.G., Wada, T.,
Mirtsos, C., Takada, H., Wakeham, A., Itie, A., Li, S., Penninger, J.M.,
Wesche, H., Ohashi, P.S., Mak, T.W. and Yeh, W.C.
Severe impairment of interleukin-1 and Toll-like receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (08-NOV-2001) Biology I, South San Francisco, CA 94080, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li,S., Strelow,A.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          signalling in mice lacking IRAK-4
Nature 416 (6882), 750-756 (2002)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 60
                                                        ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT 84
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DDRYNGHIRRESALLQTGKSFTSELLEDWGTLTKTPVQNLEQSYMPPDSSS PENKSLEV
DDRYNGHIRRESALLQTGKSFTSELLEDWGTLTTPVQNLEQSYMPPDSSS PENKSLEV
SDTRFHSFSFYELKNVTINFDERFISVGGNKMGEGGFGVVYKGYVNNTTVAVKKLAAM
VDITTEELKQOEDQEIKVMAKCQHENLVELLGFSSDGDDLCLVYVYMPNGSLLDRLSC
LDGTPPLSWHMRCKIAQGAANGINFLHENHIHRDIKSANILLDEAFTAKISDFGLAR
ASEKFAQTVMTSNIVGTTAYMAPEALLRGBITPKSDIYSFGVVLLBIITGLFAVDEHRE
ASEKFAQTVMTSNIVGTTAYMAPEALLRGBITPKSDIYSFGVVLLBIITGLFAVDEHRE
ASEKFAQTVMTSNIVGTTAYMAPEALLRGBITPKSDIYSFANGCLHEKKNKRPDIKKV
                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="interleukin-1 receptor associated kinase
/protein_id="AAM15772.1"
/db_xref="GI:20219010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="IRAK4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="protein kinase"
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|mol_type="mRNA"
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99.7%;
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Pred. No. 3.1e-64;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 19 Row: n Column: 24
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     passed the following selection criteria: matched mRNA gi: 7705840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (31-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens,
BC013316
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Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                         /translation="MMKPITPSTYVRCLNVGLIRKLSDFIDPQEGWKKLAVAIKKPSG
DDRYNQFHIRRFEALLQTGKSPTSELLFDWGTTNCTVGDLVDLLIQNEFFAPASLLLF
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ASEKFAQTVMTSRIVGTTAYMAPEALRGEITPKSDIYSFGVVLLEIITGLPAVDEHRE
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/product="Unknown (protein for MGC:13330)"
/protein_id="AAH13316.1"
/db_xref="GI:15426432"
                                                                                                                                                                                                                                                                                                                                                                          tissue_type="Brain, primitive neuroectodermal" (clone_lib="NIH_MGC_56"
                                                                                                                                                                                                                                                                                                                             note="Vector: pDNR-LIB"
                                                                                                                                                                                                                                                                                                                                                          'lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                               clone="MGC:13330 IMAGE:4287014"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    mol_type="mRNA"
db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
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Sequence 149 from Patent
AX321132
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Homo sapiens
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                          cancer
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Patent: WO 0151641-A
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DDRYNQFHIRRFEALLQTGKSPTCELLFDWGTTNCTVGDLVDLLVQIELFAPATLLLP
DAVPQTVKSLPPREAATVAQTHGPCQEKDRTSWMPMCLEHSCEP PDSSSPDNRSVES
SDRTPHSFSFHELKSITNNPDEQPASAGGINNFSWMPMCLEHSCEP PDSSSPDNRSVES
SDTRFHSFSFHELKSITNNPDEQPASAGGINNFSWMPMCLEHSCEP
STEELKQQPDQBIKVMATCQHENLVELLGFSDSDNLCLVYAYMPNGSLLDRLSC
LDGTPPLSWHTRCKVAQGTANGIRFLHENHHIHRDIKSANILLLDKDFTAKISDFGLAR
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PQLLLD1KEE1EDEEKT1EDYTDEKMSDADPASVEAMYSAASQCLHEKKNRRPD1AKV
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/protein_id="CAC60091.1"
/db_xref="GI:15386465"
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Eutheria;
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/db_xref="taxon:10095"
/note="murine IL-1 receptor-associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (08-NOV-2001) Biology South San Francisco, CA 94080, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li,S., Strelow,A., Fontana,E.J. and Wesche,H. IRAK-4: a novel member of the IRAK family with the properties of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1, (bases 1 to 1542)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF445803 TAF445803.1 GI:20219011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCT
                                                                                                                                                              GAATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTTGTGGATCTTTTG
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                                                                                                                                                                                                                                                                                     AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
                                                                               ATCCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCC 294
                                                                                                                                                                                                                                   AATCAGTTCCATATAAGGAGATTCGAAGCCTTACTTCAGACCGGGAAGAGCCCCACCTGT
                                                                                                                                                                                                                                                                                                                                       CAAGAAGGGTGGAAGAATTAGCAGTAGCTATCAAAAAGCCCGTCCGGCGACGACAGATAC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                         ACATACATACGCAACCTTAATGTGGGGATCCTTAGGAAGCTGTCGGATTTTATTGATCCT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 1542)
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a 392 c
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DAVPQTVKSLPPREAATVAQTHGPCGEKDRTS VMPMPKLEHSCENPTS SSPDNRS VES
SDTRFHS FSFHELKS I INNEDEDPASAGGINKVEEGGFGVVYKGCVNNTI VAVKKLGAN
VEISTEELKQOPDGI KVMATCQHENLVELLGFSSDSDNLCLVYAYMPNGSLLDRLSC
LOGTPPLSWHTRCKVAQGTANGI RFLHENHHI HRD IT KSANILLKDFTARI SDFGLAR
BARLAQTVMTSRI VGTTAYMAPEALAGEI TPFSDI VSFGVVLLELITGLAAVDENRE
RSARLAQTVMTSRI VGTTAYMAPEALAGEI TPFSDI VSFGVVLLELITGLAAVDENRE
RSARLAQTVMTSRI VGTTAYMAPEALAGEI TPFSDI VSFGVVLLELITGLAAVDENRE
POLLLDIKEEI EDEEKTI EDYTDEKMSDADPASVEAMYSAASQCLHEKKURRPDIAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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/note="protein kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Irak4"
|63. .1542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MNKPLTPSTYIRNLNVGILRKLSDFIDPQEGWKKLAVAIKKPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.5%;
81.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 204.4; DB 10;
Pred. No. 8.6e-42;
D; Mismatches 56;
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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
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AUTHORS
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BC051676
LOCUS
                                                                                                                                                                                   FEATURES
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VERSION
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MEDLINE
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S. W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAK Plate: 111 Row: i Column: 20
                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., García, A.M., Lu, X., Hulyk, S.W., J
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M.,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Yulan Piao and Minoru Ko
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Minoru Ko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (30-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC051676 2431 bp mRNA linear ROD 10-JUN-2003 Mus musculus interleukin-1 receptor-associated kinase 4, transcript variant 1, mRNA (cDNA clone MGC:60994 IMAGE:30017484), complete
                                                                                                                                                                           This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 239-Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: BCM-HGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                            /mol_type="mRNA"
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                                                                                                                              organism="Mus musculus"
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Sutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                        criteria: matched mRNA gi: 23943897
                                                                                                                                                                                                                                                                                information can be for http://image.llnl.gov
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Loulseged, H., Nanavati,

be found

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RESULT 14
AY186092
LOCUS
                                                                                                                                               REFERENCE
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ORIGIN
                           COMMENT
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Best Local S
Matches 238
                                                                  TITLE
JOURNAL
                                                                                                                            AUTHORS
                                                                                                                                                                                                           ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT 180
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Rieder, M.J., Armel, T.Z., Carrington, D.P., Ozuna, M., Kuldanek, S.A., Rajkumar, N., Toth, E.J., Yi, Q. and Nickerson, D.A.
Direct Submission
Direct Submission
Submitted (22-NOV-2002) Genome Sciences, University of Washington, To Cite this work please use: SeattleSNPs. NHLBI HL66682 Program for Genomic Applications, UW-FHCRC, Seattle, WA (URL:
                                                                                                                                                                                                                                                                                                 Homo sapiens interleukin-1 receptor-associated gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 μ
                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                   AY186092.1 GI:26000792
                                                                                                                                                                                                                                                                                          AY186092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACATACATACGCAACCTTAATGTGGGGATCCTTAGGAAGCTGTCGGATTTTATTGATCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCCAGATTGAGCTGTTTGCCCCCCCCCACTCTCCTGCTGCCGGATGCCGTTCCC
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ilarity 81.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAH51676.1"
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note="synonyms: NY-REN-64,
db_xref="LocusID:266632"
db_xref="MGI:2182474"
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product="interleukin-1 receptor-associated
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Pred. No. 8.1e-42;
0; Mismatches 56;
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                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 /gene="IRAK4"
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                                                                                       1025 .3915
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                     /rpt_family="Alu"
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15849. 16009,16902. 16966,20567. 20681,21130. 21239,
25244. 25427,26599. 26661,29336. 29494,29617. 31033)
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frequency="0.04"
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gene="IRAK4"
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                      frequency="0.01"
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14142 TTACTTACTTTTAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                           243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 TCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCTGA 182
                                                                                                                                                                                                      Homo sapiens 12 BAC RP11-210N13 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
AC093012
AC093012.9 GI:21629105
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 118572)

Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
                                                                                                                                                              Homo sapiens
                                                                                                                                                                           Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.6%; Score 151.8; DB 9; llarity 95.7%; Pred. No. 1.6e-28; Conservative 0; Mismatches 7;
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variation

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gene="IRAK4"

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variation

variation

repeat_region

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variation

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frequency="0.01" replace="g"

variation

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variation

variation

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variation

repeat_region

frequency="0.31" replace=""

frequency="0.02" replace="a" 972 gene="IRAK4"

variation

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REFERENCE
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AUTHORS
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davy, Carroll, L., Dederich, D.A., Davis, C., Davy, Carroll, L., Dederich, D.A., Devis, C., Davy, Carroll, L., Dederich, D.A., Devis, C., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Doubthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Escotto, M., Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorreil, J.H., Guevara, W., Gunaratne, P., Hale, S., Gill, R., Gorreil, J.H., Guevara, W., Gunaratne, P., Hale, S., Gill, R., Gorreil, J.H., Guevara, W., Gunaratne, P., Hale, S., Gill, R., Gorreil, J.H., Devara, W., Gunaratne, P., Hale, S., Gill, R., Gorreil, J.H., Devara, W., Gunaratne, P., Hale, S., Gill, R., Gorreil, J.H., Guevara, W., Gunaratne, P., Hale, S., Gill, R., Gorreil, J.H., Guevara, W., Gunaratne, P., Hale, S., Gill, R., Gorreil, J.H., Guevara, W., Gunaratne, P., Hale, S., Gill, R., Gorreil, J.H., Guevara, W., Gunaratne, P., Hale, S., Gill, R., Gorreil, J.H., Guevara, W., Gunaratne, P., Hale, S., Gill, R., Gorreil, J.H., Guevara, W., Gunaratne, P., Hale, S., Karlson, E., Kolly, S., Khan, U., Kurshi, J., Luker, J., Jay, Y., Khan, U., Kurshi, J., Luker, J., Jay, Y., Karlson, E., Karlson, E., Kelly, S., Karlson, E., Kelly, S., Karlson, E., Kelly, S., Karlson, E., Kelly, S., Karlson, E., Karls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (21-JUN-2002) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 118572)
Direct Submission
Submitted (24-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                     Submitted (03-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-JUN-2002) Human Genome Seq
of Molecular and Human Genetics, Baylor
Baylor Plaza, Houston, TX 77030, USA
6 (bases 1 to 118572)
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Baylor Plaza, Houston,
4 (bases 1 to 118572)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (04-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-AUG-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 [bases 1 to 118572]
                                                                                                                            Worley, K.C.
                                                                                                                                                             of Molecular and Human
Baylor Plaza, Houston,
7 (bases 1 to 118572)
                                                                                                                                                                                                                                                                                                                                                          Worley, K.C.
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Worley, K.C.
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lor College
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REFERENCE

JOURNAL

AUTHORS TITLE

JOURNAL

REFERENCE

TITLE JOURNAL

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Baylor Plaza, Houston, TX 77030, USA On Jun 29, 2002 this sequence version replaced gi:21535906. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Features listing. Overlapping clones are noted at the beginning and end of the

## ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome of a local database that includes entries local mapping efforts. Res. from 7:541-550) searches dbSTS, GDB, and

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rathan 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht

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FEATURES
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                                                         38216 ATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTGAT 38275
                                                                           183 ATTACTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTTTGAT 242
                 243 CCAAAATGAATTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGAT 285
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Search completed: January 18, 2004, 00:16:05 Job time: 1518 secs

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US-09-601-091-1
US-09-601-091-3
US-09-38-395A-51
US-09-887-586A-51
US-09-887-582B0-1
US-09-985-752-51
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Sequence 10, Appl

Sequence 3, Appli

Sequence 51, Appl

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Sequence 51, Appl

Sequence 51, Appl

Sequence 90, Appl

Sequence 90, Appli

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Sequence 10, Appli

Sequence 104, Appli

Sequence 1614, Appli

Sequence 120, Appli

Sequence 1, Appli
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Sequence 22, App Sequence 2, Appl		24,	Sequence 172, App	4, 1	-	Sequence 35, Appl	•	Sequence 35, App	Sequence 34, App	Sequence 34, App	-	•	•	•	Sequence 20, App	Sequence 20, App

#### DZA 3 8

ALIGNMENTS

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APPLICANT: Scanlan, Matthew
APPLICANT: Stockert, Pisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Old, Lloyd
APPLICANT: Much, Alex
TITLE OF INVENTION: Uses Therefor
FILE REFERENCE: L0461/7051
CURRENT APPLICATION NUMBER: US/09/166,350A
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: US 09/166,350
EARLIER FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
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Best Local Similarity
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                                                                                                                   194
                                                                                                                                        121 AATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCT
                                                                                                                                                                                      294;
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US-09-601-091-1
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LENGTH: 1879
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Best Local Similarity 50.5%;
Matches 98; Conservative
  Query Match
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TITLE OF INVENTION: Germacrene C Synthase
FILE REFERENCE: 4630-55758
CURRENT APPLICATION NUMBER: US/09/601,091
CURRENT FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: PCT/US99/02133
PRIOR FILING DATE: 1999-02-02
                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/601,091
CURRENT FILLING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: PCT/US99/02133
PRIOR FILING DATE: 1999-02-02
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PRIOR FILING DATE: 1998-02-02
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Colby, S. M. et al.
TITLE OF INVENTION: Germacrene C Synthase Gene of Lycopersicon
FILE REFERENCE: 4630-55758
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                                                                                                                                                                                                   SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/073,579
PRIOR FILING DATE: 1998-02-02
                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (32)..(1678)
                                                                                                              ORGANISM: Lycopersicon
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Pred. No. 0.0042;
0; Mismatches 96;
Score 40.4;
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Length 2024;
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LENGTH: 2024
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Patent No. 646877
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APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/398,395A
CURRENT FILING DATE: 1999-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
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PRIOR APPLICATION NUMBER: 60/100,993
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                                                                                                                                                                                                                                                                                                                                                                   PEATURE:
NAME/KEY: CDS
LOCATION: (32)...(1675)
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0; Mismatches 9
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Pred. No. 0.
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         CURRENT APPLICATION NUMBER: US/09/895,752
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
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Patent No. 6559
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Best Local Similarity
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SEQ ID NO 51
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APPLICANT: No. 65592971,
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APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/887,586A
CURRENT FILING DATE: 2001-06-22
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APPLICANT: No. 6495.
APPLICANT: Starks,
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NUMBER OF SEQ ID NOS: 58
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NO. 6495354
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No. 64953541, Joseph
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nilarity 50.5%;
Conservative (
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Pred. No. 0.
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Mismatches
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; NAME/KEY: CDS
; LOCATION: (32)...(1675)
; OTHER INFORMATION: VFNT germacrene C synthase US-09-903-012B-51
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                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/903,012B
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR APPLICATION DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
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APPLICANT: No. 65696561, J
APPLICANT: Starks, Courtney
APPLICANT: Manna, Kathleen
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: SYNTHASES
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TYPE: DNA
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                                                                                                                                                                                                                                                                                             TYPE: DNA
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105 TGGTGATGATACAATCAGTTTCACATAAGGAGTTTGAAGCATTACTTCAAACTGG
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Similarity 50.5%;
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Manna, Kathleen
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                                                                                                                     Conservative
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                                                                                                                     Score 40.4; DB 4
Pred. No. 0.0043;
0; Mismatches 9
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Pred. No. 0.0043;
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US-08-961-527-90/c
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US-08-545-528D-1/c
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No. 6420135
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SOFTWARE: PatentIn vers
SEQ ID NO 1
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TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome,
Patent No. 6537773
TITLE OF INVENTION: Thereof, and Uses Thereof
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                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Charles Kunsch
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CURRENT APPLICATION NUMBER: US/08/545,528D
CURRENT FILING DATE: 1995-10-19
PRIOR APPLICATION NUMBER: US 08/488,018
PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE:
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ORGANISM: Mycoplasma
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OPERATING SYSTEM: MSDC
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
                                                                                                                                                 ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
                                                  COMPUTER:
                                                                  MEDIUM TYPE:
                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                   TLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
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                                                                3.50 inch, 1.4Mb storage
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Pred. No. 4.
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US-09-734-674-3/c
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APPLICANT: WEI, Ming-Hui et al
APPLICANT: WEI, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09734674 Patent No. 6498022
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                                                                                               Query Match
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CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(202001)
                                                                                                                                                                                                  ORGANISM: Human FEATURE:
                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                    ENGTH: 202001
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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PRIOR APPLICATION DATA:
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91622 AAGAGAGTAACAAAAATTAGCTGTACCTATAAAATACACTAAGGGGGAAAAGATATACC 91563
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                      37 AAGCTGTCAGATTTTATTGATCCTCAAGAAGGATGGAAGAAGTTAGCTGTAGCTATTAAA 96
                                                                                 Similarity
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                                                                                 Score 32.8; D
Pred. No. 6.2;
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Pred. No. 0
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RESULT 12
US-09-791-211-10/c
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; NAME/KEY: CDS
; LOCATION: (22)...(1500)
US-09-096-731A-1
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                                                                                                                                                                                                                SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/09791211 Patent No. 6448080 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FASTSEQ for Windows Version 3.0 SEQ ID NO 1 LENGTH: 1728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                NAME/KEY: unsure
LOCATION: 24962
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 64383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/072,324
PRIOR FILING DATE: 1998-01-23
NUMBER OF SEQ ID NOS: 44
SOPTWARE.
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                                                                                                                                                                                                                                                                                       APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RTS-0205
                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: CSHL97-07pA
CURRENT APPLICATION NUMBER: US/09/096,731A
CURRENT FILING DATE: 1998-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hengartner, Michael O.
APPLICANT: Bogaert, Thierry Andre Oliver Eddy
APPLICANT: Van Criekinge, Wim Maria Rene
TITLE OF INVENTION: ENGULPMENT GENE AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Liu, Qiong
APPLICANT: Hengartne
                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Caenorhabditis elegans
                    OTHER INFORMATION: unknown
                                                                                                                                                                             TYPE: DNA
  NAME/KEY:
                                                                                                                                                                                                JENGTH: 98844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 11.1%;
Local Similarity 51.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1132 GATTCGTTTGATCCCAGAGCTGGAGAAAAAAAAGAGCACTGCAGCTGAGTATAATCCATTC 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1252 GAACTTCTCGCTTCTGAAGCAAT 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 AAAAGTCCCACTTCTGAATTACT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 GATTTTATTGATCCTCAAGAAGGATGGAAGAAGTTAGCTGTAGCTATTAAAAAACCATCT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74;
unsure
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Best Local Similarity 53.1%;
Matches 69; Conservative
                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Walker, Michael G. TITLE OF INVENTION: BONE REMO
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OTHER INFORMATION: u
NAME/KEY: unsure
LOCATION: 89049
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NAME/KEY: misc feature
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No.
                                                                                                                                                                                                                                                                                                                 LENGTH: 4402
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: unknown OTHER INFORMATION:
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NAME/KEY: unsure
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OTHER INFORMATION:
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                                                                                                                                                                                            Local
                                   2831 ATATTACTTGCACGAAGTACTTGATGTATGGTTATCCTGAAATTTCGGAGTATTTGGTGT
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                                                                    170 GTCCCACTT--CTGAATTACTGTTTTGACTGGGGCACCACAATTTGCACAGTTGGTGATCT 227
                                                                                                                                        110 ATGATAGATACAATCAGTTTCACATAAGGAGTTTGAAGCATTACTTCAAACTGGAAAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171
228 TGTGGATCTTTTGATCCAAAATGAATTTTTTTGCTCCTGCGAGTCTTTTGCTCCCAGATGC 287
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                                                                                                                                                                             l Similarity
97; Conserv
                                                                                                       ATAACATATGAAATTCAGTTAAAAGAATGTGTGTTTCATAATGACTTTTAACTGGTAAAA
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Volkmuth, Wayne
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Pred. No. 6.2;
0; Mismatches
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Pred. No. 2
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                                                                                                                                                                             88; Indels
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US-09-107-532A-3535
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Patent No. 6583275
GENERAL INFORMATION:
                                                                                                                                                                 Matches
                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (781)893-5007
TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3535;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                       , match 10.9%;
Local Similarity 52.2%;
les 71; Conservative
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MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                 1559
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                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...2274
SEQUENCE DESCRIPTION: SEQ ID NO: 3535:
                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2891
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1619 AAGGAAAATACGAAGGTCAGCGGTTCAATGCAAGCAAAGTAGCATATGGTGATTTGAGAA 1678
                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                        90
                                                                                                         30 AATTAGGAAGCTGTCAGATTTTATTGATCCTCAAGAAGGATGGAAGAAGTTAGCTGTAGC 89
                                TATTAAAAAACCATCTGGTGATGATAGATACAATCAGTTTCACATAAGGAGATTTGAAGC 149
                                                                             TTGTCCC 2957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1614
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US-09-134-001C-1614
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                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1614
LENGTH: 1557
                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LYNN DOUCETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND
TITLE OF INVENTION: EPIDERMIDIS FOR
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1679
1212 GATTTTCTCCGGACTACAATCTGCGGATCGTATCATGCAAGAAGAAATTTTTTGGACCAG 1270
                                                                                                                                                               1092 AGTAATTAATCAAAACAATTTGATAAAATCAAAAATTATATTGAAATTGGTAAAAAAGA
                                      207 AAATTGCACAGTTGGTGATCTTGTGGATCTTTTGATCCAAAATGAATTTTTTTGCTCCTG 265
                                                                                                                    147 AGCATTACTTCAAACTGGAAAAAGTCCCACTTCTGAATTACTGTTTGACTGGGGCACCAC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 ATTACTTCAAACTGGA 165
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                                                                           AGGCANACTAGAGACTGGTGGAACAGATGATTCTACCGGTTATTTCATTGAACCAAC
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Pred. No. 1
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Search completed: January 18, Job time : 55 secs 2004, 00:40:18